

SEQUENCE LISTING

<110> GRAFF, JONATHAN M.
MUNSTER, MATTHEW
ALLAN, DEBORAH

<120> METHODS TO IDENTIFY SIGNAL SEQUENCES

<130> UTSD:772US

<140> UNKNOWN

<141> 2001-10-31

<150> 60/300,309

<151> 2001-06-21

<160> 324

<170> PatentIn Ver. 2.1

<210> 1

<211> 884

<212> DNA

<213> Homo sapiens

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<222> (608)..(884)

<223> N = A, C, G or T/U

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265

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 20 25 30
 Ala Leu Cys Met Phe Val Ala Ala Ala Gly Ala Tyr Val His Met Val
 35 40 45
 Thr His Phe Ile Gln Ala Gly Leu Leu Ser Ala Leu Gly Ser Leu Ile
 50 55 60
 Leu Met Ile Trp Leu Met Ala Thr Pro His Ser His Glu Thr Glu Gln
 65 70 75 80
 Lys Arg Leu Gly Leu Leu Ala Gly Phe Ala Phe Leu Thr Gly Val Gly
 85 90 95
 Leu Gly Pro Ala Leu Glu Phe Cys Ile Ala Val Asn Pro Ser Ile Leu
 100 105 110
 Pro Thr Ala Phe Met Gly Thr Ala Met Ile Phe Thr Cys Phe Thr Leu
 115 120 125

Ser Ala Leu Tyr Ala Arg Arg Arg Ser Tyr Leu Phe Leu Gly Gly Ile
 130 135 140

Leu Met Ser Ala Leu Ser Leu Leu Leu Ser Ser Leu Gly Asn Val
 145 150 155 160

Phe Phe

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 20 25 30

Tyr Phe Leu Phe Thr Phe Tyr Ile Phe Val His Ile Val Arg Val Ser
 35 40 45

His Phe Ser Arg Met Thr Lys Pro Ala Phe Gly Ala Phe Ser Val Leu
 50 55 60

Leu Leu Thr Leu Leu Val Val Pro Cys Ser Leu Ser Gln Arg Arg Lys
 65 70 75 80

Lys Thr Leu Lys Lys Gln Lys Gln Gln Lys Asn Asn Leu Ile Pro Ser
 85 90 95

Ile Pro Val Thr Phe Leu Cys Met Tyr Leu Ala Val Leu Val Val Gly
 100 105 110

Leu Tyr Glu Met Val Lys Lys Ala Lys Asp Lys Arg Phe Leu Phe Phe

115 120 125
 Ser Phe Phe Val Tyr Glu Val Ala Val Tyr Phe Phe Trp Pro Gly Ser
 130 135 140

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 <212> DNA
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 tcacacaatt ttcccctatt acctggtgca aaatgactca tcacttcca aaagcttctt 420
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 <212> PRT
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 Phe Glu Lys Lys Leu Leu Gly Ser Asp Glu Ser Phe Cys Thr Arg Gly
 20 25 30
 Lys Ile Val Pro Pro Ala Asn Thr Met Val Ile Ser Trp Ser Arg Lys
 35 40 45
 His Leu Gly Val Val Val Ile Pro Ser Val Phe Cys Val Leu Val Leu
 50 55 60
 Pro Phe Leu Asn Thr Val Leu Phe Glu Ser Phe Glu Tyr Ile His Ile
 65 70 75 80
 Leu Leu Lys Pro Asn Lys Phe Arg Leu Leu Ser Ser Ser Val Leu His
 85 90 95
 Ala Thr Leu Asn Leu Pro Lys Ser Ser Ile Val Thr Tyr Met Met Ser
 100 105 110
 Trp Ala Phe Ser Glu Pro Trp Arg Thr Leu Lys Gly Arg Ile Ala Ala
 115 120 125

Phe Leu Lys Gln Ile Gly Phe Leu Met Ser Phe Gly Ser Pro Cys Leu
 130 135 140

Leu Leu Met Leu Gly Ser
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 <222> (615)..(757)
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 gagcagctgg tcagctgggg actggctcct cgacagaaag gcctggaact cctgctctct 360
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 ccaagccagc agccccacta cttgctcctt gatcctgacc gggatgtgtg cctagcgggg 540
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Gly Xaa Leu Gly Leu Xaa Gly Xaa Pro Val Arg Glu His Pro Xaa Arg
 35 40 45

Arg Pro Gly Xaa Arg Val Leu Leu Ala Pro Trp Ala Pro Pro Gln Ser
 50 55 60

Pro Arg Arg Pro Glu Leu Pro Asp Leu Ala Xaa Glu Pro Arg Ala His
 65 70 75 80
 Ile Pro Val Arg Ile Lys Glu Gln Val Val Gly Leu Leu Ala Trp Asn
 85 90 95
 Asn Cys Ser Cys Glu Ser Ser Gly Gly Gly Leu Pro Leu Pro Phe Gln
 100 105 110
 Lys Gln Val Arg Ala Ile Asp Leu Thr Lys Ala Phe Asp Pro Ala Glu
 115 120 125
 Leu Arg Ala Ala Ser Ala Thr Arg Glu Gln Glu Phe Gln Ala Phe Leu
 130 135 140
 Ser Arg Ser Gln Ser Pro Ala Asp Gln Leu Leu Ile Ala Pro Ala Asn
 145 150 155 160
 Ser Pro Leu Gln Tyr Pro Leu Gln Gly Val Glu Val Gln Pro Leu Arg
 165 170 175
 Ser Ile Leu Val Pro Gly Leu Ser Leu Gln Ala Ala Ser Gly Gln Glu
 180 185 190
 Val Tyr Gln Val Asn Leu Thr Ala Ser Leu Gly Thr Trp Asp Val Ala
 195 200 205
 Gly Glu Val Thr Gly Val Thr Leu Thr Gly Glu Gly Gln Ala Asp Leu
 210 215 220
 Thr Leu Val Ser Pro Gly Leu Asp Gln Leu Asn Arg Gln Leu Gln Leu
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 245 250 255

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<210> 12

<211> 159
 <212> PRT
 <213> Homo sapiens

<400> 12

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Glu Phe Ala Ala Ala Ser Thr Ala Phe Pro Ala Pro Pro Arg Gly Lys
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Gly Gly Asp Glu Lys Met Val Leu Leu Thr Ala Val Leu Leu Leu Leu
      20             25             30

Ala Ala Tyr Ala Gly Pro Ala Gln Ser Leu Gly Ser Phe Val His Cys
      35             40             45

Glu Pro Cys Asp Glu Lys Ala Leu Ser Met Cys Pro Pro Ser Pro Leu
      50             55             60

Gly Cys Glu Leu Val Lys Glu Pro Gly Cys Gly Cys Cys Met Thr Cys
      65             70             75             80

Ala Leu Ala Glu Gly Gln Ser Cys Gly Val Tyr Thr Glu Arg Cys Ala
      85             90             95

Gln Gly Leu Arg Cys Leu Pro Arg Gln Asp Glu Glu Lys Pro Leu His
      100            105            110

Ala Leu Leu His Gly Arg Gly Val Cys Leu Asn Glu Lys Ser Tyr Arg
      115            120            125

Glu Gln Val Lys Ile Glu Arg Asp Ser Arg Glu His Glu Glu Pro Thr
      130            135            140

Thr Ser Glu Met Ala Glu Glu Thr Tyr Ser Pro Pro Pro Gly Ser
      145            150            155

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aaaattcatt gtgtatatta ctacaaagac aaccccaaac caattttttt cctgcgaagt 240
ttaatgatcc acaagtgtat atatgaaatt ctctccttc cttgcccccc tctctttctt 300
ccctctttcc cctccagaca ttctagtttg tggagggtta tttaaaaaaa caaaaaagga 360
agatggtcaa gtttgtaaaa tatttgtttg tgctttttcc ccctccttac ctgacccctt 420
acgagtttac aggtctgtgg caatactctt aaccataaga attgaaatgg tgaagaaaca 480

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gatagcagat gtcttttaaat gaaatacatg tatattgngt atggacttaa ttatgcacat 660
gctcagatgt gtagacatcc tncgnatatt tacataacat atngaggtaa tagatagggg 720
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cctttggggc ttttttacc ccaanatggn ccttggggaat caaattcctt nnggaaatgg 840
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<213> Homo sapiens

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<223> XAA = ANYTHING

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Met Xaa His Gly Leu Phe Ser Lys Xaa Lys Lys Xaa Lys Phe Xaa Xaa
      20              25              30

Gly Pro Phe Pro Xaa Gly Ile Phe Pro Arg Xaa Xaa Leu Gly Val Lys
      35              40              45

Lys Ala Gln Arg Val Trp Gly Pro Xaa Asn Leu Arg Ser Lys Gln Xaa
      50              55              60

Leu Glu Asn Xaa Ser Arg Tyr Ile Pro Leu Ser Ile Thr Ser Ile Cys
      65              70              75              80

Tyr Val Asn Xaa Arg Arg Met Ser Thr His Leu Ser Met Cys Ile Ile
      85              90              95

Lys Ser Ile Xaa Asn Ile His Val Phe His Leu Lys Thr Ser Ala Ile
      100              105              110

Cys Met Tyr Gln Lys Cys Lys Leu Arg Ser Lys Trp Leu Cys Leu Ser
      115              120              125

Val Tyr Val Leu Leu Tyr Xaa Ser Ser Ile Val Phe Gln Tyr Phe Glu
      130              135              140

Pro Leu Val Tyr Thr Cys Phe Phe Thr Ile Ser Ile Leu Met Val Lys
      145              150              155              160

Ser Ile Ala Thr Asp Leu Thr Arg Arg Gly Ser Gly Lys Glu Gly Glu
      165              170              175

Lys Ala Gln Thr Asn Ile Leu Gln Thr Pro Ser Ser Phe Phe Val Phe

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180 185 190

Leu Asn Asn Pro Pro Gln Thr Arg Met Ser Gly Gly Glu Arg Gly Lys
195 200 205

Lys Glu Arg Gly Ala Arg Lys Glu Glu Asn Phe Ile Tyr Thr Leu Val
210 215 220

Asp His Thr Ser Gln Glu Lys Asn Trp Phe Gly Val Val Phe Val Val
225 230 235 240

Ile Tyr Thr Met Asn Phe Glu Tyr Asn Asn Lys Val Thr Val Phe Cys
245 250 255

Thr Gly Gly Lys Val Val His Glu Lys Asn Lys Asn Ser Cys Trp Asp
260 265 270

Phe Ile Met Leu Leu Thr Val Trp Phe Val Trp Phe Cys Leu Leu Leu
275 280 285

Ile Phe Ser Leu Leu Leu Pro Ala Trp Leu Cys Gln Thr Asn Gln Gly
290 295 300

Ser
305

<210> 15
<211> 613
<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

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 Trp Arg Ser Cys Phe Pro Asp His Ser Cys Gly Glu Leu Gly Val Glu
 35 40 45
 Gln Arg Ser Phe Cys Ile Gln Leu Pro Arg Gln Arg Arg Met Gly Ser
 50 55 60
 Pro Gln Pro Glu Glu Arg His Asp Arg Ile Lys Thr Arg Cys Gln Gly
 65 70 75 80
 Val Asp Gly Arg Lys Arg Pro Leu Gly Pro Gly Lys Asn Asp Arg Gly
 85 90 95
 Ala Gly Pro Pro Leu Glu Gly Ser Ala Arg Pro Ala Val Met Ala Lys
 100 105 110
 Leu Arg Ser Pro Gly Arg Gln Pro Arg Arg Pro Glu Arg Lys Pro Pro
 115 120 125
 Pro Gln Arg Ser Thr Ser Arg Val Gly Val Arg Arg Ser Gln Arg Val
 130 135 140
 Lys Val Arg Arg Pro Met His Gln Lys Arg Pro Lys Leu Ser Arg Asn
 145 150 155 160
 Ser Leu Gly His Ser Leu Pro Pro Ile Trp Ile Ala Trp Thr Gly Gly
 165 170 175
 Ala Leu Met Met Met Ala Ala Ala Thr Leu Gly Ile Ser Thr Arg Thr
 180 185 190
 Thr Glu Ala Arg Pro Pro Gly Ser
 195 200

<210> 17
 <211> 284
 <212> DNA
 <213> Homo sapiens

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<210> 18
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 18
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 Ser Thr Leu Asp Trp Cys Glu Glu Asn Tyr Ser Val Thr Trp Tyr Ile
 35 40 45
 Ala Glu Phe Trp Asn Thr Val Ser Asn Leu Ile Met Ile Ile Pro Pro
 50 55 60
 Met Phe Gly Ala Ile Gln Ser Val Arg Asp Gly Leu Glu Lys Arg Tyr
 65 70 75 80
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<210> 19
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 <212> DNA
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 <222> (662)..(919)
 <223> N = A, C, G or T/U

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 cactgtgact gtgtccattc attggcttag gtatagtctg gcttttaaga agatgtaaaa 180
 gcaaactatt gttagcagct tgttttatat tgtttctttc cagtgaagttc ttataacctg 240
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 ccntagcacc ttaaaacctt ctnccttttt aaagaatctg gctggaggcc taatccttgn 840
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<210> 20
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<221> MOD_RES
 <222> (3)..(93)
 <223> XAA = ANYTHING

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 20 25 30

Pro Pro Ala Arg Phe Phe Lys Lys Xaa Glu Gly Phe Lys Val Leu Xaa
 35 40 45

Cys Gly Ser Ser Pro Leu Lys Xaa Phe Gly Glu Arg Lys Val Lys Leu
 50 55 60

Arg Ser Lys Ala Phe Glu Xaa Ser Xaa Asp Asn Xaa His Gln Arg Val
 65 70 75 80

Ala Glu Ser Xaa His His Val Asp Lys Val Asp Gln Xaa Ser Val Thr
 85 90 95

Arg Cys His Val Leu Gln Asp Tyr Arg Leu Leu Gln Ala Trp Trp Lys
 100 105 110

Lys Gly Leu Val Leu Pro Pro His Leu Asn Leu Val Leu Leu Val Ala
 115 120 125

Ser His Tyr Phe Cys Gln Ala Lys Pro Ile Cys Ser Ser Ile Leu Glu
 130 135 140

Asn Thr Leu Lys Arg Lys Met Gln Ile Lys Gln Gln Val Lys Asp Leu
 145 150 155 160

Leu Leu Trp Pro Asp Cys Lys Lys Met Ala Arg Arg Met Leu Ala Val
 165 170 175

Thr Ser Ser Gln Lys Glu Cys Gln Ala Ile Leu Met Val Arg Gln Glu
 180 185 190

His His Gln Ala Asn Trp Leu Ala Lys Val Val Leu Gln Cys Phe Lys
 195 200 205

Ile Gln Trp Val Ser Phe Leu Leu Pro Leu Lys Met Gln Val Ile Arg
 210 215 220

Thr His Trp Lys Glu Thr Ile Asn Lys Leu Leu Thr Ile Val Cys Phe
 225 230 235 240

Tyr Ile Phe Leu Lys Ala Arg Leu Tyr Leu Ser Gln Met Asp Thr Val
 245 250 255

Thr Val Arg Glu Glu Ala Phe Leu Arg Lys Val Val His Leu Gln Leu
 260 265 270

Leu Met Asn Ile Gln Ile Thr Ile Leu Val Leu Gln Met Thr Ala Val
 275 280 285

Val Met Lys Val Leu Ile Pro Thr Gly Ser
 290 295

<210> 21
 <211> 563
 <212> DNA
 <213> Homo sapiens

<400> 21
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 gtatagtagg agacaagcag ctacaagaca agatctccca agtcctccat agcagtgtat 120
 taagggtttt cggtaatttt taaggcaggt tgtaagctct tccattattt cacagcagct 180
 ggctatgtca ggagtcacct catctgcgat tggatgatga tgggtgataa ttccacattg 240
 ctggtagaga tccagaagggt ttgggaactct atattttgac agttcccctc tgggtgcagaa 300
 aacaaatatg tcttgtatac cacagctctt tagttcttct gtatcttttt ggacatttct 360
 tctaacatct ttaaattttac aacctggaag agcacataaa ccgagaaaact gagaacaatt 420
 cactcgtgac aaagatagcc atgatatatg aattggagtc tgttcattct caataggctc 480
 ttcattctgat gagtcaaact cacttggttg tattgaactg ggcggcttca tcgctggccc 540
 gccgtcgacg cggccgcgaa ttc 563

<210> 22
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 22
 Ile Arg Gly Arg Val Asp Gly Gly Pro Ala Met Lys Pro Pro Ser Ser
 1 5 10 15
 Ile Gln Thr Ser Glu Phe Asp Ser Ser Asp Glu Glu Pro Ile Glu Asp
 20 25 30
 Glu Gln Thr Pro Ile His Ile Ser Trp Leu Ser Leu Ser Arg Val Asn
 35 40 45
 Cys Ser Gln Phe Leu Gly Leu Cys Ala Leu Pro Gly Cys Lys Phe Lys
 50 55 60
 Asp Val Arg Arg Asn Val Gln Lys Asp Thr Glu Glu Leu Lys Ser Cys
 65 70 75 80
 Gly Ile Gln Asp Ile Phe Val Phe Cys Thr Arg Gly Glu Leu Ser Lys
 85 90 95
 Tyr Arg Val Pro Asn Leu Leu Asp Leu Tyr Gln Gln Cys Gly Ile Ile
 100 105 110
 Thr His His His Pro Ile Ala Asp Gly Gly Thr Pro Asp Ile Ala Ser
 115 120 125

Cys Cys Glu Ile Met Glu Glu Leu Thr Thr Cys Leu Lys Asn Tyr Arg
 130 135 140

Lys Thr Leu Ile His Cys Tyr Gly Gly Leu Gly Arg Ser Cys Leu Val
 145 150 155 160

Ala Ala Cys Leu Leu Leu Tyr Leu Ser Asp Thr Ile Ser Pro Glu Gln
 165 170 175

Ala Ile Asp Ser Leu Arg Asp Leu Arg Gly Ser
 180 185

<210> 23
 <211> 171
 <212> DNA
 <213> Homo sapiens

<400> 23
 ggatcctgga tgccacgaga tggcaagagc cacaatcaat gaatgcatta tgggtcaaac 60
 ttttcatgta tatggatgtg actattttta caaataaaaag aagtgaaaag ttaaaaaaaaa 120
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa agtcgacgcg gccgcgaatt c 171

<210> 24
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 24
 Glu Phe Ala Ala Ala Ser Thr Phe Phe Phe Phe Phe Phe Phe Phe Phe
 1 5 10 15

Phe Phe Phe Leu Thr Phe His Phe Phe Tyr Leu Leu Lys Ser His Pro
 20 25 30

Tyr Thr Lys Asp Leu Thr Ile Met His Ser Leu Ile Val Ala Leu Ala
 35 40 45

Ile Ser Trp His Pro
 50

<210> 25
 <211> 678
 <212> DNA
 <213> Homo sapiens

<400> 25
 ggatcctgca cttatccagg ttaagatcta aataggctgt aagtttcttg ttaaagtcac 60
 gaacaatgtt ggcaggatca ctatctgcaa actctgggac aggcacactg ataaattcaa 120
 cttcttcttc ttcaaagatt ttaatatctt cttcaattgt ctggtagaga gcagctgggg 180
 catctgcaga gggctcattt aagatgacat catctttgat gtactttatt ccacagtagt 240
 acacgtcatc tggttgaagt gcaaaatatt tgtacaagta tgctcctcct agaataacac 300

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ctgcaagcat aaatgctagt ccaaagcaca tgcaccaaca ccaggctctt ctttggccaa 360
ctggtaccac atcatctggg tccttgcaagt ccaccgcgac ggcgtcgggg gggatgatga 420
gcgcctcctc gccgctcttg ggctcgctct tcttggcctc cttctggggc agagcggagt 480
tgaacgtcac cttcaccatg gcgcggcctg gggcgccctc gaagggcggc ggcgggtcgg 540
ggcgcggctg cggctcccgg ctgcgattgc agcctctacg gncgggctcc gggagccggc 600
tncgggcggc tgaagaaggt cggaagctt cgcggcggca gaagcggcta ctgcgggtcg 660
acgccggccg cgaaattc                                     678

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<210> 26
<211> 219
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (33)
<223> XAA = ANYTHING

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<400> 26
Glu Phe Arg Gly Arg Arg Arg Pro Ala Val Ala Ala Ser Ala Ala Ala
 1             5             10             15

Lys Leu Pro Asp Leu Leu Gln Pro Pro Xaa Ala Gly Ser Arg Ser Pro
      20             25             30

Xaa Val Glu Ala Ala Ile Ala Ala Gly Ser Arg Ser Arg Ala Pro Ser
      35             40             45

Arg Arg Arg Pro Ser Arg Ala Pro Gln Ala Ala Pro Trp Arg Arg Ser
      50             55             60

Thr Pro Leu Trp Pro Arg Arg Arg Pro Arg Arg Thr Ser Pro Arg Ala
      65             70             75             80

Ala Arg Arg Arg Ser Ser Ser Pro Pro Thr Pro Ser Arg Trp Thr Ala
      85             90             95

Arg Thr Gln Met Met Trp Tyr Gln Leu Ala Lys Glu Glu Pro Gly Val
      100             105             110

Gly Ala Cys Ala Leu Asp His Leu Cys Leu Gln Val Leu Phe Glu Glu
      115             120             125

His Thr Cys Thr Asn Ile Leu His Phe Asn Gln Met Thr Cys Thr Thr
      130             135             140

Val Glu Ser Thr Ser Lys Met Met Ser Ser Met Ser Pro Leu Gln Met
      145             150             155             160

Pro Gln Leu Leu Ser Thr Arg Gln Leu Lys Lys Ile Leu Lys Ser Leu
      165             170             175

Lys Lys Lys Lys Leu Asn Leu Ser Val Cys Leu Ser Gln Ser Leu Gln
      180             185             190

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Ile Val Ile Leu Pro Thr Leu Phe Met Thr Leu Thr Arg Asn Leu Gln
 195 200 205

Pro Ile Ile Leu Thr Trp Ile Ser Ala Gly Ser
 210 215

<210> 27
 <211> 916
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (651)..(915)
 <223> N = A, C, G, or T/U

<400> 27
 ggatcctagg acaaagccac atcccaaata cttgctgaga gcagtggcta caaatgttaa 60
 catgagatta gacattgaga tgggtcccttt atattgagag aacatggact ttggagttgg 120
 gcagacttga atttgcattc tggtcttagt gggtactacc tagtgtggct ttgagctatt 180
 aaactttcca aagtttcgaa ggacttatct gtaacatagt aatggtaatc caccttatgg 240
 ggtagttgtc ttgaagaggc tatttgggag gctgaggcaa gaggatcact tgaggccagg 300
 aggttgaaac cagcctgggc aacacagcga gaccctgtgt ctacaaaaaa ttaaaaaatt 360
 aggcattgtg gcgtgcacct gaagtcccag ctactcaagg cagagatggg aggatcactt 420
 gtgcccagga gctccaggct gcagtgagcc atgattttgc cactgcactc cagactgggt 480
 gacagagcaa gaccccttct ctttggttggg ggcaaaaaaa aaaaaaagag ggtatatgaa 540
 gtacctagta taatatctag cctgaattgc ctataatgac gcacttcctt tctttccctt 600
 ggggttccagc tgncaaacac tcttctacaa gtaagataag cccagctttg natggtcaat 660
 ggataaacat ttcctatttc tttgtaaatc ccatnttctg cagacatctc aatttcacat 720
 ttggccaaaa aagtcctttc attccttanc cctgganaaa taacctttnt taaatnttaa 780
 accgntntgc ctgaactttg gctatcctct tntacatntc cttaaaccan ggacttggaa 840
 cttcttggat cantccaag attaattcct taantttttc anaccaaccg gtatgaagca 900
 gggaatangg ccttnt 916

<210> 28
 <211> 236
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(93)
 <223> XAA = ANYTHING

<400> 28
 Xaa Gly Xaa Ile Pro Cys Phe Ile Pro Val Gly Xaa Lys Xaa Leu Arg
 1 5 10 15

Asn Ser Trp Xaa Ser Lys Lys Phe Gln Val Xaa Gly Leu Arg Xaa Cys
 20 25 30

Xaa Arg Gly Pro Lys Phe Arg Xaa Xaa Gly Leu Xaa Phe Xaa Lys Gly

35 40 45
 Tyr Xaa Ser Arg Xaa Lys Glu Lys Asp Phe Phe Gly Gln Asn Asp Val
 50 55 60
 Cys Arg Xaa Trp Asp Leu Gln Arg Asn Arg Lys Cys Leu Ser Ile Asp
 65 70 75 80
 His Xaa Lys Leu Gly Leu Ser Tyr Leu Lys Ser Val Xaa Gln Leu Lys
 85 90 95
 Pro Lys Gly Lys Lys Gly Ser Ala Ser Leu Ala Ile Gln Ala Arg Tyr
 100 105 110
 Tyr Thr Arg Tyr Phe Ile Tyr Pro Leu Phe Phe Phe Phe Ala Pro Asn
 115 120 125
 Lys Glu Lys Gly Ser Cys Ser Val Thr Gln Ser Gly Val Gln Trp Gln
 130 135 140
 Asn His Gly Ser Leu Gln Pro Gly Ala Pro Gly His Lys Ser Ser His
 145 150 155 160
 Leu Cys Leu Glu Leu Gly Leu Gln Val His Ala Thr Met Pro Asn Phe
 165 170 175
 Leu Ile Phe Cys Arg His Arg Val Ser Leu Cys Cys Pro Gly Trp Phe
 180 185 190
 Gln Pro Pro Gly Leu Lys Ser Ser Cys Leu Ser Leu Pro Asn Ser Leu
 195 200 205
 Phe Lys Thr Thr Thr Pro Gly Gly Leu Pro Leu Leu Cys Tyr Arg Val
 210 215 220
 Leu Arg Asn Phe Gly Lys Phe Asn Ser Ser Lys Pro
 225 230 235

<210> 29
 <211> 930
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (611)..(928)
 <223> N = A, C, G or T/U

<400> 29
 ggatccgctcg gactgcacgt tgtcatagaa tgtcaagtag ccaaaaatgg cagtcaagaa 60
 gtacataaca aacatggcga aaaaggagat gtttgaaacc atctgcattt ttttctgtga 120
 tcgggtcttta agtcactgt aaattggcag gactgacggg tggcaaacaa atgcaaatgc 180
 aatggtgggt aaagcataca cggctcttga attgaaggta acatattttg gcgtacacgt 240
 gtcagcattt gttgaattag cacttattgt tgaatttagc tctggaacaa tgcaggggaat 300

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ttgaaatttc ttgtaaataa ccacaattag gaaaaaaacc atacagctca aggaaaatcc 360
actagtatag ccaagatacc ctaagttctt caagagacac agagggagaa ttatgccaaa 420
ggtaactatc accaccagaa cgcggccatc cacgtaccag gctgaaaatg tctcttcctt 480
tcccattaga aactttatgg cagagggtag ttcatTTTTT acgatgaaga ggtagctcag 540
cattgctcca gtgttctgta gagagggtggc ttcaaagatt acgaacttcc tgtgggtgcc 600
aagacttggt nccccacttt tcatacacca tgcagnctgt tcttttgaac agatcaatag 660
ganggttaat ggaatatata gacagcaatg tcactgaagt caaaagtacc cgaaaaagtn 720
gggattccag tgtttgccag ggcaaaaggc caattcccaa aattccactt gnccataatg 780
gccttgctta aggttaaaac cgacatgccc taanggaggt tgnacctggg aatatactca 840
ttncactttt ttttttccaa aggctgtttg gganantttt tttanttttc cgaccnaaat 900
aaacttgntt ttaacngacc tttttttnct 930

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<210> 30
<211> 307
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (1)..(104)
<223> XAA = ANYTHING

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<400> 30
Xaa Lys Lys Arg Ser Val Lys Xaa Lys Phe Ile Xaa Val Gly Lys Xaa
 1              5              10              15

Lys Lys Xaa Ser Gln Thr Ala Phe Gly Lys Lys Lys Val Xaa Val Tyr
      20              25              30

Ser Gln Val Gln Pro Pro Leu Gly His Val Gly Phe Asn Leu Lys Gln
      35              40              45

Gly His Tyr Gly Gln Val Glu Phe Trp Glu Leu Ala Phe Cys Pro Gly
 50              55              60

Lys His Trp Asn Pro Xaa Phe Phe Gly Tyr Phe Leu Gln His Cys Cys
 65              70              75              80

Leu Tyr Ile Pro Leu Thr Xaa Leu Leu Ile Cys Ser Lys Glu Gln Xaa
      85              90              95

Ala Trp Cys Met Lys Ser Gly Xaa Pro Ser Leu Trp His His Arg Lys
      100              105              110

Phe Val Ile Phe Glu Ala Thr Ser Leu Gln Asn Thr Gly Ala Met Leu
      115              120              125

Ser Tyr Leu Phe Ile Val Lys Asn Glu Leu Pro Ser Ala Ile Lys Phe
      130              135              140

Leu Met Gly Lys Glu Glu Thr Phe Ser Ala Trp Tyr Val Asp Gly Arg
      145              150              155              160

Val Leu Val Val Ile Val Thr Phe Gly Ile Ile Leu Pro Leu Cys Leu

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165	170	175
Leu Lys Asn Leu Gly Tyr Leu Gly Tyr Thr Ser Gly Phe Ser Leu Ser		
180	185	190
Cys Met Val Phe Phe Leu Ile Val Val Ile Tyr Lys Lys Phe Gln Ile		
195	200	205
Pro Cys Ile Val Pro Glu Leu Asn Ser Thr Ile Ser Ala Asn Ser Thr		
210	215	220
Asn Ala Asp Thr Cys Thr Pro Lys Tyr Val Thr Phe Asn Ser Lys Thr		
225	230	235
Val Tyr Ala Leu Pro Thr Ile Ala Phe Ala Phe Val Cys His Pro Ser		
245	250	255
Val Leu Pro Ile Tyr Ser Glu Leu Lys Asp Arg Ser Gln Lys Lys Met		
260	265	270
Gln Met Val Ser Asn Ile Ser Phe Phe Ala Met Phe Val Met Tyr Phe		
275	280	285
Leu Thr Ala Ile Phe Gly Tyr Leu Thr Phe Tyr Asp Asn Val Gln Ser		
290	295	300

Asp Gly Ser
305

<210> 31
<211> 919
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (610)..(918)
<223> N = A, C, G or T/U

<400> 31
gggatccggg gattaaggat ggaggggacta aattcaagat attaacaaag gaacaaagaa 60
acagggcctg atgggaggca gaggatagaa cagactgtac agtgggaata aagatcatat 120
ctatttaciaa ggaagtagaa aagacatggt aatggatata aaattgagtg tgaaacctgg 180
gaaaggacag aaaactcctc ccttttgctt gacctccttt ttactcccct accttggcct 240
gtgctatcct gagacactcc tcaattgctc aattaattct ccaggaaagg caaacctata 300
gtcaatagtt agcttggcaa gaatataggt taataattag agttggagga agctaacagt 360
ggagatagga cttgagtagc tgccactggt agttttatct ataacctctc ctggaacctc 420
gcattaacct cagatttcat tgaattaaaa agaagggtggg agggcaagta aatcaatcaa 480
aacttccata aaacaagtac cccaactgaa ctaccatcaa ttaaagtgc aactgcaggg 540
gtatatgggt ggctggggct gaggccatct aaaggccaga ggggaaaaaa tgcataatga 600
taaatacagan gatgggtacc agaactgncc cttccttcaa tcagatcaca gcagagccca 660
agatgcaggc aaccagtggg aaatcnttgg gaagactctg gggccaacc ccacgattag 720
gggaaaccct tccttaaaaa ggttgcntga aggggaaact gggccctttg aaaaagttac 780
nggaaccna gtggnccctt accttcacct tcggccatta ncttacaagg gaccttctg 840

cnggggcctg aaaattgcct cccatttta nctttaccta ggaacccctt ccnaggncaa 900
 ttgggttcc ccatggtnt 919

<210> 32
 <211> 290
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(100)
 <223> XAA = ANYTHING

<400> 32
 Xaa Pro Trp Gly Thr Gln Ile Xaa Leu Gly Arg Gly Ser Val Lys Xaa
 1 5 10 15
 Lys Trp Gly Gly Asn Phe Gln Ala Pro Ala Gly Arg Ser Leu Val Xaa
 20 25 30
 Trp Pro Lys Val Lys Val Lys Xaa His Xaa Gly Ser Xaa Asn Phe Phe
 35 40 45
 Lys Gly Pro Ser Phe Pro Phe Xaa Gln Pro Phe Gly Arg Val Ser Pro
 50 55 60
 Asn Arg Gly Val Gly Pro Gln Ser Leu Pro Xaa Asp Phe Pro Leu Val
 65 70 75 80
 Ala Cys Ile Leu Gly Ser Ala Val Ile Leu Lys Glu Gly Xaa Val Leu
 85 90 95
 Val Pro Ile Xaa Phe Ile His Met His Phe Phe Pro Ser Gly Leu Met
 100 105 110
 Ala Ser Ala Pro Ala Thr His Ile Pro Leu Gln Phe Ala Leu Leu Met
 115 120 125
 Val Val Gln Leu Gly Tyr Leu Phe Tyr Gly Ser Phe Asp Phe Thr Cys
 130 135 140
 Pro Pro Thr Phe Phe Leu Ile Gln Asn Leu Arg Leu Met Arg Gly Ser
 145 150 155 160
 Arg Arg Gly Tyr Arg Asn Tyr Gln Trp Gln Leu Leu Lys Ser Tyr Leu
 165 170 175
 His Cys Leu Pro Pro Thr Leu Ile Ile Asn Leu Tyr Ser Cys Gln Ala
 180 185 190
 Asn Tyr Leu Val Cys Leu Ser Trp Arg Ile Asn Ala Ile Glu Glu Cys
 195 200 205
 Leu Arg Ile Ala Gln Ala Lys Val Gly Glu Lys Gly Gly Gln Ala Lys

210 215 220
 Gly Arg Ser Phe Leu Ser Phe Pro Arg Phe His Thr Gln Phe Asp Ile
 225 230 235 240
 His Tyr His Val Phe Ser Thr Ser Leu Ile Gly Met Ile Phe Ile Pro
 245 250 255
 Thr Val Gln Ser Val Leu Ser Ser Ala Ser His Gln Ala Leu Phe Leu
 260 265 270
 Cys Ser Phe Val Asn Ile Leu Asn Leu Val Pro Pro Ser Leu Ile Pro
 275 280 285
 Gly Ser
 290

<210> 33
 <211> 916
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (735)..(915)
 <223> N = A, C, G OR T/U

<400> 33
 ggatccgccca tggtagcggc aaaagagttt tttctgtctc cgaggggtca ttttgatacc 60
 ctccccacgg cacagcattt cgtacttctg tctctctggc aggtaatcca cagcaacccc 120
 ttttttcttt ggtgtagttt tctgatacaga ttggatcatc gaagcagact tattgacatc 180
 ttttttctta gccattatat actcaaaata ttttaagtta ccattagctc tctgatgttc 240
 aggatctagt tcaagaagct tctttgtgag caaaagtgcc ttatccaggt ctccctgctg 300
 atataccgca tagctcaaataaatctagaac agagacttta tctatggtag aaatctcgcc 360
 ttcattccagt tgccttaggg cttgttccat ccacagttcc gtatggtaat aatctgcttc 420
 tgtataggcc actttgcccc actcaaagca gtcctcagcc cgttagaaaa gatttgtgtt 480
 tcaactctgg aagattaccc tttgagatgg tatctgtatc caaattgtag gtatcctgga 540
 gacgtaacag agctttggct gcccacacct gatcttcac attaggaaaag tactgnctct 600
 gaatgggtan ggtagagata aagccatctg acatatcctt aaggaccaga ttctccaact 660
 cacttcactc agtattcaga cgttcattaa atttgaatgc atttactggg tggcccaaca 720
 aatccttctg gaacntttgn cgctggacta agtaccgga tctaacttct ntgcccattt 780
 ttttaantggn ctacctgggc ctntntggcc ttaannnanc tttcnaaaaag cccnnaactt 840
 tncaagnntg ggcnaannng ncntttgccn ntganannaaa aacntggang nccccaanct 900
 ggaaccnaa ttnnnt 916

<210> 34
 <211> 299
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(103)

<223> XAA = ANYTHING

<400> 34

Xaa Asn Xaa Val Pro Xaa Leu Gly Xaa Ser Xaa Phe Xaa Xaa Xaa Xaa
1 5 10 15

Gln Xaa Xaa Xaa Xaa Pro Xaa Leu Xaa Lys Xaa Xaa Ala Phe Xaa Lys
20 25 30

Xaa Xaa Gly Xaa Xaa Gly Pro Gly Xaa Pro Xaa Lys Lys Trp Ala Xaa
35 40 45

Xaa Leu Asp Arg Val Thr Ser Ser Xaa Lys Xaa Ser Arg Arg Ile Cys
50 55 60

Trp Ala Thr Gln Met His Ser Asn Leu Met Asn Val Ile Leu Ser Glu
65 70 75 80

Val Ser Trp Arg Ile Trp Ser Leu Arg Ile Cys Gln Met Ala Leu Ser
85 90 95

Leu Pro Tyr Pro Phe Arg Xaa Ser Thr Phe Leu Met Met Lys Ile Arg
100 105 110

Leu Gly Gln Pro Lys Leu Cys Tyr Val Ser Arg Ile Pro Thr Ile Trp
115 120 125

Ile Gln Ile Pro Ser Gln Arg Val Ile Phe Gln Glu Asn Thr Asn Leu
130 135 140

Phe Arg Ala Glu Asp Cys Phe Glu Leu Gly Lys Val Ala Tyr Thr Glu
145 150 155 160

Ala Asp Tyr Tyr His Thr Glu Leu Trp Met Glu Gln Ala Leu Arg Gln
165 170 175

Leu Asp Glu Gly Glu Ile Ser Thr Ile Asp Lys Val Ser Val Leu Asp
180 185 190

Tyr Leu Ser Tyr Ala Val Tyr Gln Gln Gly Asp Leu Asp Lys Ala Leu
195 200 205

Leu Leu Thr Lys Lys Leu Leu Glu Leu Asp Pro Glu His Gln Arg Ala
210 215 220

Asn Gly Asn Leu Lys Tyr Phe Glu Tyr Ile Met Ala Lys Glu Lys Asp
225 230 235 240

Val Asn Lys Ser Ala Ser Asp Asp Gln Ser Asp Gln Lys Thr Thr Pro
245 250 255

Lys Lys Lys Gly Val Ala Val Asp Tyr Leu Pro Glu Arg Gln Lys Tyr
260 265 270

Glu Met Leu Cys Arg Gly Glu Gly Ile Lys Met Thr Pro Arg Arg Gln

275

280

285

Lys Lys Leu Phe Cys Arg Tyr His Gly Gly Ser
290 295

<210> 35

<211> 916

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (735)..(915)

<223> N = A, C, G, OR T/U

<400> 35

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ggatccgccgca tggtagcggc aaaagagttt tttctgtctc cgaggggtca ttttgatacc 60
ctccccacgg cacagcattt cgtacttctg tctctctggc aggtaatcca cagcaacccc 120
ttttttcttt ggtgtagttt tctgatcaga ttgggtcatct gaagcagact tattgacatc 180
tttttcttta gccattatat actcaaaata ttttaagtta ccattagctc tctgatgttc 240
aggatctagt tcaagaagct tctttgtgag caaaagtgcc ttatccaggt ctccctgctg 300
atataccgca tagctcaaat aatctagaac agagacttta tctatggtag aaatctcgcc 360
ttcatccagt tgccttaggg cttgttccat ccacagttcc gtatggtaat aatctgcttc 420
tgtataggcc actttgccca actcaaagca gtctcagcc cgtagaaaa gatttgtgtt 480
tcactcctgg aagattaccc tttgagatgg tatctgtatc caaattgtag gtatcctgga 540
gacgtaacag agctttggct gccccaacct gatcttcac attaggaaag tactgnctct 600
gaatgggtan ggtagagata aagccatctg acatatacct aaggaccaga ttctccaact 660
cacttcactc agtattcaga cgttcattaa atttgaatgc atttactggg tggcccaaca 720
aatccttctg gaacntttgn cgctggacta agttaccoga tctaacttct ntgcccattt 780
tttaantggn ctacctgggc ctntntggcc ttaannnanc tttcnaaaaag cccnnaactt 840
tncaagnntg ggcnaannng ncntttgccn ntganmnnaa aacntggang nccccaanct 900
ggaaccnaa ttnnnt 916

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<210> 36

<211> 106

<212> PRT

<213> Homo sapiens

<400> 36

Asn Ser Arg Pro Arg Arg Pro Gly Trp Leu Arg Gly Ala Ala Pro Gly
1 5 10 15

Pro Arg Gly Ser Gln Ser Asn Glu Thr Thr Ala Cys Ser Arg Leu Val
20 25 30

Glu Ile Ser Arg Arg His Gln Trp Ala Arg Ser Glu Pro Ser Gly Pro
35 40 45

Pro Val Trp Asn Gln Thr Cys Ala Arg Gly Arg Ala Val Gly Gln Arg
50 55 60

Gly Arg Gly Asp Glu Gly Ala Met Ala Arg Lys Leu Ser Val Ile Leu
65 70 75 80

Ile Leu Thr Phe Ala Leu Ser Val Thr Asn Pro Leu His Glu Leu Lys
85 90 95

Ala Ala Ala Phe Pro Gln Thr Thr Gly Ser
100 105

<210> 37
<211> 626
<212> DNA
<213> Homo sapiens
<220>
<221> modified_base
<222> (586)
<223> N = A, C, G, OR T/U

<400> 37
ggatccacca accccggcct cccaaagtgc tgggattaca ggcattgagcc accacgcca 60
gccattcctt gtcatttcta tcatttgata catctatact tctgaataat cataactgat 120
actcaaagag atgccctgac accctccaag gttctacaag gtgaccaaat cagagaggtc 180
acctcatgcc tagtattatt ttgggggttag catacatttt ataataatta ttttaaaact 240
ggcaatccat tttgggactc aatgacagct ctctctatta atcatattgt tttattaact 300
gaaatagtcc actcagtcag taggattaat gatcagagat tatgacacaa ctaaaaccaa 360
agctggggca atgggctctc agaatggaac caccattat gaactatcca tctgaccaac 420
tctttaactt tcttcctaaa tatgagatca ccaaggcggt tcaatgcagc ctgcacaatt 480
catggggcag ggctcctcaga ttaaagactt tacatttatg tagaattcaa gtatcatttt 540
tcactaagca aactctattt gctcactctc ttctacatgt aattgnccaa ctttggttga 600
ctgctgagtc ctcatgggaa gaattc 626

<210> 38
<211> 188
<212> PRT
<213> Homo sapiens

<400> 38
Ile Leu Pro Met Arg Thr Gln Gln Ser Thr Lys Val Gly Gln Leu His
1 5 10 15

Val Glu Glu Ser Glu Gln Ile Glu Phe Ala Lys Met Ile Leu Glu Phe
20 25 30

Tyr Ile Asn Val Lys Ser Leu Ile Gly Pro Cys Pro Met Asn Cys Ala
35 40 45

Gly Cys Ile Glu Thr Pro Trp Ser His Ile Glu Glu Ser Arg Val Gly
50 55 60

Gln Met Asp Ser Ser Trp Val Val Pro Phe Glu Pro Ile Ala Pro Ala
65 70 75 80

Leu Val Leu Val Val Ser Ser Leu Ile Ile Asn Pro Thr Asp Val Asp
85 90 95

Tyr Phe Ser Asn Asn Met Ile Asn Arg Glu Ser Cys His Val Pro Lys
 100 105 110

Trp Ile Ala Ser Phe Lys Ile Ile Ile Ile Lys Cys Met Leu Thr Pro
 115 120 125

Lys Tyr Ala Gly Asp Leu Ser Asp Leu Val Thr Leu Asn Leu Gly Gly
 130 135 140

Cys Gln Gly Ile Ser Leu Ser Ile Ser Tyr Asp Tyr Ser Glu Val Met
 145 150 155 160

Tyr Gln Met Ile Glu Met Thr Arg Asn Gly Trp Ala Trp Trp Leu Met
 165 170 175

Pro Val Ile Pro Ala Leu Trp Glu Ala Gly Val Gly
 180 185

<210> 39
 <211> 897
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (634)..(896)
 <223> N = A, C, G OR T/U

<400> 39
 ggatcctgag ctaagcatgg tccctccgta gatatccaga gccagctgag aataggcaaa 60
 gccaaaaaca gtgatggtca ggccggccag cagggccagc ttgagcaggg actccaagac 120
 tgcagcagcc acagcaacgt cctcctgctt ctgaagtgtg gcaccccttc ccctctccag 180
 caccttagca aaaaatatat aaaaactttc ctctattggc tggaaaatta atctggccac 240
 aagggagcca agattattca ctatatcata cacaccctga tcaccaaagt tcaatacatt 300
 caaaaatgtc atcacatatc gctcgccttc tgtcaaaatc tgtttcaaga aagactgttt 360
 gaaaaaactc caagtcagtt tagcctcttt ccagtttata aacgctccat ttcttgtaat 420
 attgggtaac agatctgtta ttctggagac aggaagagtt tgaagcttgg ttgattctgg 480
 ggaacccagt aactttgtga aataaataac atagcagagc accagaactg tggatatagaa 540
 aagctggggc aaagagaaaa tgtacaatcc ccagtgaggc aaccacagca cgagaaaagc 600
 tgtcagacgc tcttaagaat taccgcaggc tctntgcaat caccttgagc ttncaaacat 660
 atgtgcttgt gcccaagaac caaaaggctn ttctanaagc ttcaccactg gcgaaagacc 720
 aaccgnacca ntccagttgc atantgaggg acaccattag gatcngcctt tnagcagttt 780
 aaccagatcn gccccaggaat anggcccaac ttcccagggg actggttacc ancaggttaa 840
 gggctggtcc agctncttgg ggccccctgg anatgtttgn gaaggccttt ggccnnt 897

<210> 40
 <211> 296
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES

<222> (1)..(86)

<223> XAA = ANYTHING

<400> 40

Xaa Gly Gln Arg Pro Ser Gln Thr Xaa Pro Gly Gly Pro Arg Xaa Leu
1 5 10 15

Asp Gln Pro Leu Thr Xaa Trp Val Thr Val Pro Trp Glu Val Gly Pro
20 25 30

Tyr Ser Trp Ala Asp Leu Val Xaa Leu Leu Lys Gly Xaa Ser Trp Cys
35 40 45

Pro Ser Xaa Cys Asn Trp Xaa Gly Xaa Val Gly Leu Ser Pro Val Val
50 55 60

Lys Leu Xaa Glu Xaa Pro Phe Gly Ser Trp Ala Gln Ala His Met Phe
65 70 75 80

Xaa Ser Ser Arg Leu Xaa Arg Ala Cys Gly Asn Ser Glu Arg Leu Thr
85 90 95

Ala Phe Leu Val Leu Trp Leu Pro His Trp Gly Leu Tyr Ile Phe Ser
100 105 110

Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu Val Leu Cys Tyr Val Ile
115 120 125

Tyr Phe Thr Lys Leu Leu Gly Ser Pro Glu Ser Thr Lys Leu Gln Thr
130 135 140

Leu Pro Val Ser Arg Ile Thr Asp Leu Leu Pro Asn Ile Thr Arg Asn
145 150 155 160

Gly Ala Phe Ile Asn Trp Lys Glu Ala Lys Leu Thr Trp Ser Phe Phe
165 170 175

Lys Gln Ser Phe Leu Lys Gln Ile Leu Thr Glu Gly Glu Arg Tyr Val
180 185 190

Met Thr Phe Leu Asn Val Leu Asn Phe Gly Asp Gln Gly Val Tyr Asp
195 200 205

Ile Val Asn Asn Leu Gly Ser Leu Val Ala Arg Leu Ile Phe Gln Pro
210 215 220

Ile Glu Glu Ser Phe Tyr Ile Phe Phe Ala Lys Val Leu Glu Arg Gly
225 230 235 240

Lys Asp Ala Thr Leu Gln Lys Gln Glu Asp Val Ala Val Ala Ala Ala
245 250 255

Val Leu Glu Ser Leu Leu Lys Leu Ala Leu Leu Ala Gly Leu Thr Ile
260 265 270

Thr Val Phe Gly Phe Ala Tyr Ser Gln Leu Ala Leu Asp Ile Tyr Gly
 275 280 285

Gly Thr Met Leu Ser Ser Gly Ser
 290 295

<210> 41
 <211> 607
 <212> DNA
 <213> Homo sapiens

<400> 41
 ggatccgtgg ccagaaaaaa aaaaatcggt acctacaaaa tctcttgggc aacacttaag 60
 ccatggaaga gccacatga atccaggtct actttccttt acaggtagat tccagaacaa 120
 caacaaaaaa tgtaagacta caagaaatga tttaatatga taaaactccc atttcaaaac 180
 ccagttctaa aggatttacn tgactaatgc ntgattattt agtcatggaa aatgtctctc 240
 ataaaagtgc tcctaacaaa acatgatcta caataattta taaaatgtga agggttggga 300
 tgtgcagact gattgggtgca cgtcagggtt tttctcttaa ataaggata aaaaactatg 360
 atatcatagt ctttcgactt tattttctga gataaaaaag tataggcata ggtgttttta 420
 atagtcttct tgatgatatc ctttagaata atctatcaa tggcttcttt catgtttcct 480
 gattatcagc attcatcagt gttactgtca gccttgatta agtggttgaa aatttcagag 540
 aagaataagc aactttctgtg aacctttccc caatccctga gaatcatgtc gacgcggccg 600
 cgaattc 607

<210> 42
 <211> 189
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (121)
 <223> XAA = ANYTHING

<400> 42
 Asn Ser Arg Pro Arg Arg His Asp Ser Gln Gly Leu Gly Lys Gly Ser
 1 5 10 15
 Gln Lys Leu Leu Ile Leu Leu Asn Phe Gln Pro Leu Asn Gln Gly Gln
 20 25 30
 His Met Leu Ile Ile Arg Lys His Glu Arg Ser His Leu Ile Asp Tyr
 35 40 45
 Ser Lys Gly Tyr His Gln Glu Asp Tyr Lys His Leu Cys Leu Tyr Phe
 50 55 60
 Phe Ile Ser Glu Asn Lys Val Glu Arg Leu Tyr His Ser Phe Leu Tyr
 65 70 75 80
 Leu Ile Glu Lys Gln Pro Asp Val His Gln Ser Val Cys Thr Ser Gln
 85 90 95

Pro Phe Thr Phe Tyr Lys Leu Leu Ile Met Phe Cys Glu His Phe Tyr
100 105 110

Glu Arg His Phe Pro Leu Asn Asn Xaa Ala Leu Val Xaa Ile Leu Asn
115 120 125

Trp Val Leu Lys Trp Glu Phe Tyr His Ile Lys Ser Phe Leu Val Val
130 135 140

Leu His Phe Leu Leu Leu Phe Trp Asn Leu Pro Val Lys Glu Ser Arg
145 150 155 160

Pro Gly Phe Met Trp Ala Leu Pro Trp Leu Lys Cys Cys Pro Arg Asp
165 170 175

Phe Val Gly Asn Asp Phe Phe Phe Ser Gly His Gly Ser
180 185

<210> 43

<211> 466

<212> DNA

<213> Homo sapiens

<400> 43

ggatccttta atgtcctcat ttgttgtctg gttggagctg atcaagtagg tgtggaatcc 60
tgagaggcca acgatggacc agacagagaa gaagcacacc acagcctcca ggacgcttgc 120
aggactgtcc ttaagggcat ttaggaatcc tgtttgcgtg gaacgaagaa tgacgtgggt 180
gataacgaat gcaaataataa agactgtcag aaaagacaga gataaaataa acatataaaa 240
aaatctgtag ttctttttcc ccacacagtt gcctaccagc ggacagtggg gatcaaaccg 300
ttctacgcag ttatcacaaa ggctgcaatg ggaggcgcgga gggggccgga aaatcttgca 360
ggtgaaacag tatttaagtt tcacggtctg gccattgatg atgacttctt tgggttctggg 420
aggcggggcgg taccctccctg aactgggtcg acgcggccgc gaattc 466

<210> 44

<211> 153

<212> PRT

<213> Homo sapiens

<400> 44

Asn Ser Arg Pro Arg Arg Pro Ser Ser Gly Gly Tyr Arg Pro Pro Pro
1 5 10 15

Arg Thr Lys Glu Val Ile Ile Asn Gly Gln Thr Val Lys Leu Lys Tyr
20 25 30

Cys Phe Thr Cys Lys Ile Phe Arg Pro Pro Arg Ala Ser His Cys Ser
35 40 45

Leu Cys Asp Asn Cys Val Glu Arg Phe Asp His His Cys Pro Trp Val
50 55 60

Gly Asn Cys Val Gly Lys Arg Asn Tyr Arg Phe Phe Tyr Met Phe Ile
65 70 75 80

Leu Ser Leu Ser Phe Leu Thr Val Phe Ile Phe Ala Phe Val Ile Thr
85 90 95

His Val Ile Leu Arg Ser Gln Gln Thr Gly Phe Leu Asn Ala Leu Lys
100 105 110

Asp Ser Pro Ala Ser Val Leu Glu Ala Val Val Cys Phe Phe Ser Val
115 120 125

Trp Ser Ile Val Gly Leu Ser Gly Phe His Thr Tyr Leu Ile Ser Ser
130 135 140

Asn Gln Thr Thr Asn Glu Asp Ile Lys
145 150

<210> 45
<211> 395
<212> DNA
<213> Homo sapiens

<400> 45
ggatcctgtg acaatctgat ggccatacca ggagcaagct accaaggcgg caagacctgc 60
cacgatgaaa attatgcctc caccatggc tatacgggcc ttcttcactt tgctgtctcc 120
cccacagcgc agtgcacttc atgcccacg tggccacaaa catggccagg aagcccagca 180
ccaggagac caccattagg gctcgagtgg cctgcaaggc cgcggacagg gcgagcaccg 240
agtcgtacat tttgcagctc atcatccccg tgctctgcgt gacgcagtcc atccacagcc 300
ccttgtacat ggcctgggcc gtgatgatgt tgtcaccgc ataggagctc atctgccact 360
gcgggatggc ggtgcgtcga cgcggccgcg aattc 395

<210> 46
<211> 126
<212> PRT
<213> Homo sapiens

<400> 46
Ile Arg Gly Arg Val Asp Ala Pro Pro Ser Arg Ser Gly Arg Ala Pro
1 5 10 15

Met Arg Val Thr Thr Ser Ser Arg Pro Arg Pro Cys Thr Arg Gly Cys
20 25 30

Gly Trp Thr Ala Ser Arg Arg Ala Arg Gly Ala Ala Lys Cys Thr Thr
35 40 45

Arg Cys Ser Pro Cys Pro Arg Pro Cys Arg Pro Leu Glu Pro Trp Trp.
50 55 60

Ser Pro Trp Cys Trp Ala Ser Trp Pro Cys Leu Trp Pro Arg Trp Ala
65 70 75 80

Ser Ala Leu Arg Cys Gly Gly Asp Asp Lys Val Lys Lys Ala Arg Ile
85 90 95

Ala Met Gly Gly Gly Ile Ile Phe Ile Val Ala Gly Leu Ala Ala Leu
 100 105 110

Val Ala Cys Ser Trp Tyr Gly His Gln Ile Val Thr Gly Ser
 115 120 125

<210> 47
 <211> 597
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (7)..(594)
 <223> N = A, C, G OR T/U

<400> 47
 ggatccnanc tncnnacacn nacagagatc gacgnnnnct accaggtgag ccattgcggt 60
 aatatggact ttattnaagt aagttactta tattactgcc ttncataca ctatntaatn 120
 ncatttgaat tactgagaga ctaatatgcc atgtctaaaa ctgtctcttt cataagtaat 180
 tttgngcctn cngctacncc aagcnaagnc aactcttctt tttttatata ctatganatg 240
 gcnccgangg cgaggagaaan gctgaangnc tncgaactgg cagcggngan accgganngn 300
 acnangaagc gggnnnnccn ttcgengcca nntctttgg nnttatcacg gnnagccanc 360
 gctnnggnct gatagcgntc cgncncaccc agccggccan agtcgatgaa tccnaaaaag 420
 cggccatttt ccaccatgan attcggcaag caggcatcgc catgggtcac gacganatcc 480
 tcgcccgcgg gcatgcncgc cttgagcctg gcgaacagtt cggntggcgc gagcccctga 540
 tgctnttcgn ccaaatcatc ctgatcgaca agaccggctt ccatccgagn acngngct 597

<210> 48
 <211> 192
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (2)..(192)
 <223> XAA = ANYTHING

<400> 48
 Ser Xaa Xaa Ser Asp Gly Ser Arg Ser Cys Arg Ser Gly Phe Gly Arg
 1 5 10 15

Xaa Ala Ser Gly Ala Arg Ala Xaa Arg Thr Val Arg Gln Ala Gln Gly
 20 25 30

Xaa His Ala Arg Arg Arg Gly Xaa Arg Arg Asp Pro Trp Arg Cys Leu
 35 40 45

Leu Ala Glu Xaa His Gly Gly Lys Trp Pro Leu Phe Xaa Ile His Arg
 50 55 60

Leu Trp Pro Ala Gly Xaa Xaa Gly Xaa Leu Ser Xaa Xaa Ser Xaa Gly

65	70	75	80
Xaa Pro Xaa Gln Arg Xaa Trp Xaa Arg Xaa Gly Xaa Pro Leu Xaa Xaa			
	85	90	95
Xaa Xaa Arg Xaa Xaa Arg Cys Gln Phe Xaa Xaa Xaa Gln Xaa Ser Pro			
	100	105	110
Arg Xaa Arg Xaa His Xaa Ile Val Tyr Lys Lys Gly Arg Val Xaa Xaa			
	115	120	125
Ala Ser Xaa Ser Xaa Arg Xaa Lys Ile Thr Tyr Glu Arg Asp Ser Phe			
	130	135	140
Arg His Gly Ile Leu Val Ser Gln Phe Lys Xaa Xaa Xaa Ile Val Tyr			
	145	150	155
Gly Lys Ala Val Ile Val Thr Tyr Xaa Asn Lys Val His Ile Thr Ala			
	165	170	175
Met Ala His Leu Val Xaa Xaa Val Asp Leu Cys Xaa Cys Xaa Xaa Xaa			
	180	185	190

<210> 49
 <211> 547
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (538)
 <223> N = A, C, G OR T/U

<400> 49
 ggatccccac aaacacacag gactccctcc ctcccacaga gaacacaaag ttgttaactg 60
 aagaacaaga taaataatat gctagtccat ttactgatt ttaaagatac tgcaattttt 120
 atacatttcg atgatttttc aacatttttg agctgtttgg ctttgcagca cagcaattca 180
 tacactatac ntgtacaaaa ttaccagcaa gactggaatg atgtattaat agaaggcacc 240
 atcatgctta ttacattacc agagaacaaa aatacagtaa agacaatttt cactgtacac 300
 agcttaaaga aaggaaaaaa ggggaggagg agtgtgttga gcagccagcc atccctgtac 360
 tgaagagggg caggtagaaa aatccttagat atggagctac taaatctggc ctaatagtca 420
 agaccatcgc atttgaagtt ctaattttta ttatttagtt cataactaaa atgatttcct 480
 tctggaatat acttgtagtc ttgttaaggt ttatgtgtac acacgctgtc gacgcggncg 540
 cgaattc 547

<210> 50
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 50

Asn Ser Arg Pro Arg Arg Gln Arg Val Tyr Thr Thr Leu Thr Arg Leu
1 5 10 15

Gln Val Tyr Ser Arg Arg Lys Ser Phe Leu Thr Lys Lys Leu Glu Leu
20 25 30

Gln Met Arg Trp Ser Leu Leu Asp Gln Ile Leu His Ile Asp Phe Ser
35 40 45

Thr Cys Pro Ser Ser Val Gln Gly Trp Leu Ala Ala Gln His Thr Pro
50 55 60

Pro Pro Leu Phe Ser Phe Leu Ala Val Tyr Ser Glu Asn Cys Leu Tyr
65 70 75 80

Cys Ile Phe Val Leu Trp Cys Asn Lys His Asp Gly Ala Phe Tyr Tyr
85 90 95

Ile Ile Pro Val Leu Leu Val Ile Leu Tyr Xaa Tyr Ser Val Ile Ala
100 105 110

Val Leu Gln Ser Gln Thr Ala Ala Lys Cys Lys Ile Ile Glu Met Tyr
115 120 125

Lys Asn Cys Ser Ile Phe Lys Ile Ser Lys Met Asp His Ile Ile Tyr
130 135 140

Leu Val Leu Gln Leu Thr Thr Leu Cys Ser Leu Trp Glu Gly Gly Ser
145 150 155 160

Pro Val Cys Leu Trp Gly Ser
165

<210> 51

<211> 742

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (512)..(741)

<223> N = A, C, G OR T/U

<400> 51

ggatcctgag tcaagccaaa aaaaaaaaaa aaacccaaac aaaacaaaaa aaacaaataa 60
agccatgcca atctcatctt gttttctgcg caagtttaggt tttgtcaaga aaggggtgtaa 120
cgcaacttaa gtcatagtcc gcctagaagc atttgcggtg gacgatggag gggccggact 180
cgtcatactc ctgcttgctg atccacatct gctggaaggt ggacagcgag gccaggatgg 240
agccgccgat ccacacggag tacttgcgct caggaggagc aatgatcttg atcttcattg 300
tgctgggtgc cagggcagtg atctccttct gcatcctgtc ggcaatgcca ggggtacatgg 360
tggtgccgcc agacagcact gtgttggcgt acaggtcttt gcggatgtcc acgtcacact 420
tcatgatgga gttgaaggta gtttcgtgga tgccacagga ctccatgccc aggaaggaag 480
gctggaagag tgcctcaggg cagcgggaacc gntcattgcc aatggtgatg acctggccgt 540

caggcancct cgtanctctt ctncagggag gagctggaan cagccgtggc catttcttgc 600
 tcgaagtcca gcgncgacgt accnntaccn tntccttant gcctaccccn cgatttcccc 660
 gctcgntcgn nntngtccnn ancnnntccc centtcttgg nncgnntnct cnnnnngcgn 720
 nncgcnngn ntcnncttn nt 742

<210> 52
 <211> 243
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(62)
 <223> XAA = ANYTHING

<400> 52
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Glu Xaa Xaa Xaa Xaa Glu
 1 5 10 15
 Xaa Gly Xaa Xaa Xaa Gly Xaa Xaa Arg Xaa Ser Gly Glu Ile Xaa Gly
 20 25 30
 Ala Xaa Arg Xaa Xaa Xaa Xaa Tyr Val Xaa Ala Gly Leu Arg Ala Arg
 35 40 45
 Asn Gly His Gly Xaa Phe Gln Leu Leu Pro Xaa Glu Glu Xaa Arg Gly
 50 55 60
 Cys Leu Thr Ala Arg Ser Ser Pro Leu Ala Met Xaa Gly Ser Ala Ala
 65 70 75 80
 Leu Arg His Ser Ser Ser Leu Pro Ser Trp Ala Trp Ser Pro Val Ala
 85 90 95
 Ser Thr Lys Leu Pro Ser Thr Pro Ser Ser Val Thr Trp Thr Ser Ala
 100 105 110
 Lys Thr Cys Thr Pro Thr Gln Cys Cys Leu Ala Ala Pro Pro Cys Thr
 115 120 125
 Leu Ala Leu Pro Thr Gly Cys Arg Arg Arg Ser Leu Pro Trp His Pro
 130 135 140
 Ala Gln Arg Ser Arg Ser Leu Leu Leu Leu Ser Ala Ser Thr Pro Cys
 145 150 155 160
 Gly Ser Ala Ala Pro Ser Trp Pro Arg Cys Pro Pro Ser Ser Arg Cys
 165 170 175
 Gly Ser Ala Ser Arg Ser Met Thr Ser Pro Ala Pro Pro Ser Ser Thr
 180 185 190
 Ala Asn Ala Ser Arg Arg Thr Met Thr Val Ala Leu His Pro Phe Leu
 195 200 205

Thr Lys Pro Asn Leu Arg Arg Lys Gln Asp Glu Ile Gly Met Ala Leu
 210 215 220

Phe Val Phe Phe Val Leu Phe Trp Phe Phe Phe Phe Phe Trp Leu Asp
 225 230 235 240

Ser Gly Ser

<210> 53
 <211> 598
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (214)..(597)
 <223> N = A, C, G OR T/U

<400> 53
 ggatcctttc actgagtatt tgtcaggggc acactgggtgg caagaagttt ctccttttatt 60
 tgaataagag ttggctgggc aaagtttgca gaaagaggag ccttgcttgt ctgcatacgt 120
 gccaggtttg caggggaagc attctgaagt gtaggccacc cctgttatgg caatgtttct 180
 caccagcaca ggcttgggta ctttgggtcca tacntgagaa ggctgtgggt ctccaataga 240
 ggacattatt gcctcgattt agctccacac tgtggaattc ccatcctttc tctgtgggtct 300
 tcatccacct ggagtcacct gcattgggct ggcactgggc attctgaacg aaaaactcaa 360
 agatgatgct ggagtctgga tagtagtatt cgaagttaac ggtgccagat tgcttcagggt 420
 tgacggcgta catcagtgtg gctgtgcatt cgtccgtggt ggaggcgatg tagtcgcccc 480
 ggggaaccca cttggacgaa gtacagttcc cgggtggactc agcagcactg tcatccagct 540
 ccatgntggc tgagaggctg gcanagccat gggncanntc atcccactca tcanacnc 598

<210> 54
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(124)
 <223> XAA = ANYTHING

<400> 54
 Xaa Xaa Met Ser Gly Met Xaa Xaa Pro Met Ala Xaa Pro Ala Ser Gln
 1 5 10 15
 Pro Xaa Trp Ser Trp Met Thr Val Leu Leu Ser Pro Pro Gly Thr Val
 20 25 30
 Leu Arg Pro Ser Gly Phe Pro Gly Ala Thr Thr Ser Pro Pro Thr Arg
 35 40 45
 Thr Asn Ala Gln Pro His Cys Thr Pro Ser Thr Ser Asn Leu Ala Pro

50 55 60
 Leu Thr Ser Asn Thr Thr Ile Gln Thr Pro Ala Ser Ser Leu Ser Phe
 65 70 75 80
 Ser Phe Arg Met Thr Ser Ala Ser Pro Met Gln Met Thr Pro Gly Gly
 85 90 95
 Arg Pro Gln Arg Lys Asp Gly Asn Ser Thr Val Trp Ser Ile Glu Ala
 100 105 110
 Ile Met Ser Ser Ile Gly Glu Pro Gln Pro Ser Xaa Val Trp Thr Lys
 115 120 125
 Val Pro Lys Pro Val Leu Val Arg Asn Ile Ala Ile Thr Gly Val Ala
 130 135 140
 Tyr Thr Ser Glu Cys Phe Pro Cys Lys Pro Gly Thr Tyr Ala Asp Lys
 145 150 155 160
 Gln Gly Ser Ser Phe Cys Lys Leu Cys Pro Ala Asn Ser Tyr Ser Asn
 165 170 175
 Lys Gly Glu Thr Ser Cys His Gln Cys Asp Pro Asp Lys Tyr Ser Val
 180 185 190
 Lys

<210> 55
 <211> 657
 <212> DNA
 <213> Homo sapiens

<400> 55
 ggatcccatg aggtagtcgg tcaggtcccg gccagccagg tccagacgca ggatggcgtg 60
 ggggagggcg tagccctcgt agatgggcac cgtgtgggtg acccgcctc cagagtccat 120
 gacaatgccg gtggtgcgcc cagaggcgta gagggacagc acggcctgga tggccacgta 180
 catggccggg gtgttgaagg tctcaaact aatctgagtc atcttctctc tgttggcctt 240
 ggggttcagg ggggcctcgg tcagcagcac tgggtgctcc tccggggcca cgcgagctc 300
 gttgtagaag gtgtggtgcc agatcttctc catgtcgtcc cagttggtga cgatgccatg 360
 ctcaatgggg tacttcaggg tcaggatgcc acgcttgctc tgggcctcgt cgcccacgta 420
 ggagtccttc tggcccatgc ccaccatgac gccctggtgt ctggggcgcc cgacgatgga 480
 aggaaacacg gctcggggag cgtcgtcccc agcaaaacca gctttgcaca tgccggagcc 540
 attgtcaatg accagcgcg cgtatctctt ttccattgcg accggcagag aaacgcgcgg 600
 cggagcggcg gaagaacaga gtgcgagagt tggcagcgtc gacgcggccg cgaattc 657

<210> 56
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 56

Glu Phe Ala Ala Ala Ser Thr Leu Pro Thr Leu Ala Leu Cys Ser Ser
 1 5 10 15
 Ala Ala Pro Pro Arg Val Ser Leu Pro Val Ala Met Glu Glu Glu Ile
 20 25 30
 Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met Cys Lys Ala Gly Phe
 35 40 45
 Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro Ser Ile Val Gly Arg
 50 55 60
 Pro Arg His Gln Gly Val Met Val Gly Met Gly Gln Lys Asp Ser Tyr
 65 70 75 80
 Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile Leu Thr Leu Lys Tyr
 85 90 95
 Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp Asp Met Glu Lys Ile
 100 105 110
 Trp His His Thr Phe Tyr Asn Glu Leu Arg Val Ala Pro Glu Glu His
 115 120 125
 Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu
 130 135 140
 Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn Thr Pro Ala Met Tyr
 145 150 155 160
 Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr
 165 170 175
 Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr His Thr Val Pro Ile
 180 185 190
 Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu Arg Leu Asp Leu Ala
 195 200 205
 Gly Arg Asp Leu Thr Asp Tyr Leu Met Gly Ser
 210 215

<210> 57

<211> 237

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> (211)..(232)

<223> N = A, C, G OR T/U

<400> 57

ggatcccacc ttcaacacct tacaagtaaa gacaatgaag aacagttgaa acatgcaaaa 60

tatggagctt ttcattgtaat tactcttttta ctgtttacca ttcactataa ttcacaatta 120
 aaattgtgtg actaaacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 180
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaggg ngganaggnc gacncggccg cnaattc 237

<210> 58
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (2)..(8)
 <223> XAA = ANYTHING

<400> 58
 Glu Xaa Ala Ala Xaa Ser Xaa Xaa Pro Pro Phe Phe Phe Phe Phe Phe
 1 5 10 15
 Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe
 20 25 30
 Phe Cys Leu Val Thr Gln Phe Leu Ile Ile Val Asn Gly Lys Gln Lys
 35 40 45
 Ser Asn Tyr Met Lys Ser Ser Ile Phe Cys Met Phe Gln Leu Phe Phe
 50 55 60
 Ile Val Phe Thr Cys Lys Val Leu Lys Val Gly Ser
 65 70 75

<210> 59
 <211> 199
 <212> DNA
 <213> Homo sapiens

<400> 59
 ggatccctgg ctgccttctt catccgagga cgccgaggcc aagctcagca gcaccgcaca 60
 cagcagcagc gtcagcccta tccggaccgc catctctctc tcggggcccg tgccaacccc 120
 tagagctgtc gccttcgcct ctgccaccac ggactcagcc accaccgccg cctcgcccg 180
 tcgacgcggc cgcgaattc 199

<210> 60
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 60
 Asn Ser Arg Pro Arg Arg Arg Gly Glu Ala Ala Val Val Ala Glu Ser
 1 5 10 15
 Val Val Ala Glu Ala Lys Ala Thr Ala Leu Gly Val Gly Thr Gly Pro
 20 25 30

Glu Arg Arg Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Cys Ala
 35 40 45

Val Leu Leu Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln
 50 55 60

Gly Ser
 65

<210> 61
 <211> 489
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (456)..(489)
 <223> N = A, C, G OR T/U

<400> 61
 ggatccggca accatgacca gcgagaccac caccagggca ccaaagagga tcttggtgag 60
 gcagttcact tccaagtcga acaggccgat cttacttcgg ggatttgagg tattcatgac 120
 actccggagt tctctgccag tgtaaagaac aacaccacaca acagtacctg atgcgaccac 180
 agtgccagcc cacagcgtgt tctctatgct caggctctcg ctgacgggg ggtcgctgtc 240
 ttctcgggta aaagttccca cgaagttgtg aatgtcaata tttggctctt ctgcgtacac 300
 atacgatcga atctgaagaa ggtcggcggc cgtggggagc ctctgcgtgc aggccacggg 360
 aagccgcagc ttccagtcgg tctccccatc cagctgatcc gtccgcaaga agcatgaccc 420
 gtttttttct gatgtectca ggaagatcat gtcggnnggg acccgctggt cgangcggcc 480
 nccaattcn 489

<210> 62
 <211> 163
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(12)
 <223> XAA = ANYTHING

<400> 62
 Xaa Ile Gly Gly Arg Xaa Asp Gln Arg Val Pro Xaa Asp Met Ile Phe
 1 5 10 15

Leu Arg Thr Ser Glu Lys Asn Gly Ser Cys Phe Leu Arg Thr Asp Gln
 20 25 30

Leu Asp Gly Glu Thr Asp Trp Lys Leu Arg Leu Pro Val Ala Cys Thr
 35 40 45

Gln Arg Leu Pro Thr Ala Ala Asp Leu Leu Gln Ile Arg Ser Tyr Val
 50 55 60

Tyr Ala Glu Glu Pro Asn Ile Asp Ile His Asn Phe Val Gly Thr Phe
65 70 75 80

Thr Arg Glu Asp Ser Asp Pro Pro Ile Ser Glu Ser Leu Ser Ile Glu
85 90 95

Asn Thr Leu Trp Ala Gly Thr Val Val Ala Ser Gly Thr Val Val Gly
100 105 110

Val Val Leu Tyr Thr Gly Arg Glu Leu Arg Ser Val Met Asn Thr Ser
115 120 125

Asn Pro Arg Ser Lys Ile Gly Leu Phe Asp Leu Glu Val Asn Cys Leu
130 135 140

Thr Lys Ile Leu Phe Gly Ala Leu Val Val Val Ser Leu Val Met Val
145 150 155 160

Ala Gly Ser

<210> 63
<211> 392
<212> DNA
<213> Homo sapiens

<400> 63
ggatccgagt gctgatttgt acattgattc aggggagtaa ttggggagaa ggaaaaaggt 60
ggggtggaat gctggctcgg cctgcccagt cacatgggtg gcagcagggc agctcagagg 120
ttgcctgaag agttcgtttt tcttgctcca gtccatctgc aggggcccgt ttgctgctgc 180
gtttctgggtg ggccctctct ttggccatgg ccagggagat gttgaagtct aggatggggt 240
cggaggagga ggtagaccgag ggcgctgtgg agtcctgttt tggggggctg tcttggnaat 300
tcagctcctc gctggtgtca ctggaggcgg atctcaccag ggctggcctg gggctctcca 360
aggctgcctc tggtcgacgc ggccgcgaat tc 392

<210> 64
<211> 127
<212> PRT
<213> Homo sapiens

<400> 64
Ile Arg Gly Arg Val Asp Gln Arg Gln Pro Trp Arg Ala Pro Gly Gln
1 5 10 15

Pro Trp Asp Pro Pro Pro Val Thr Pro Ala Arg Ser Ile Xaa Lys Thr
20 25 30

Ala Pro Gln Asn Arg Thr Pro Gln Arg Pro Arg Leu Pro Pro Pro Pro
35 40 45

Thr Pro Ser Thr Ser Thr Ser Pro Trp Pro Trp Pro Lys Arg Gly Pro
50 55 60

Thr Arg Asn Ala Ala Ala Asn Gly Pro Leu Gln Met Asp Trp Ser Lys
65 70 75 80

Lys Asn Glu Leu Phe Arg Gln Pro Leu Ser Cys Pro Ala Ala Thr His
85 90 95

Val Thr Gly Arg Ala Glu Pro Ala Phe His Pro Thr Phe Phe Leu Leu
100 105 110

Pro Asn Tyr Ser Pro Glu Ser Met Tyr Lys Ser Ala Leu Gly Ser
115 120 125

<210> 65
<211> 577
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (551)..(575)
<223> N = A, C, G OR T/U

<400> 65
ggatcctttc acaaaccag caaccatcac aaacagaagg acgagaatat taacagctgt 60
gaagacttta ttcacccaag cagactcttt tactccaaaa gacaaaagac ctgctagaag 120
taatataagg cacacagcaa aaaaatcggg atattctgca agaccagtgt aattcattct 180
gaagtatgtc ctcaaaaact gaccaatctg ttgctaaga agttcatcaa aggtgccact 240
ccaggctctt gcaacacttg atgtacctat cacatacgat aaaatgagat tccagccagt 300
gatgaaggcc cacagctctc cgacagtcac gtaggtgtac aaatatgcag acccgtctt 360
gggaacacgg gccccaaatt cggcatagca gaggccagcc atcactgaag ccagggcagc 420
aatgaggaag gacaccacga tgctggggcc cgagtctgcc ttggccacct cccagcgag 480
gacataaacc ccggccccaa ggggtacttc aacgcccagg gcaatgaggt ccatggtgga 540
taagcagcgg nataatttgg ngnnntntan actgncc 577

<210> 66
<211> 192
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (1)..(9)
<223> XAA = ANYTHING

<400> 66
Xaa Ser Xaa Xaa Xaa Xaa Lys Leu Xaa Arg Cys Leu Ser Thr Met Asp
1 5 10 15

Leu Ile Ala Leu Gly Val Gly Ser Thr Leu Gly Ala Gly Val Tyr Val
20 25 30

Leu Ala Gly Glu Val Ala Lys Ala Asp Ser Gly Pro Ser Ile Val Val

35 40 45
 Ser Phe Leu Ile Ala Ala Leu Ala Ser Val Met Ala Gly Leu Cys Tyr
 50 55 60
 Ala Glu Phe Gly Ala Arg Val Pro Lys Thr Gly Ser Ala Tyr Leu Tyr
 65 70 75 80
 Thr Tyr Val Thr Val Gly Glu Leu Trp Ala Phe Ile Thr Gly Trp Asn
 85 90 95
 Leu Ile Leu Ser Tyr Val Ile Gly Thr Ser Ser Val Ala Arg Ala Trp
 100 105 110
 Ser Gly Thr Phe Asp Glu Leu Leu Ser Lys Gln Ile Gly Gln Phe Leu
 115 120 125
 Arg Thr Tyr Phe Arg Met Asn Tyr Thr Gly Leu Ala Glu Tyr Pro Asp
 130 135 140
 Phe Phe Ala Val Cys Leu Ile Leu Leu Leu Ala Gly Leu Leu Ser Phe
 145 150 155 160
 Gly Val Lys Glu Ser Ala Trp Val Asn Lys Val Phe Thr Ala Val Asn
 165 170 175
 Ile Leu Val Leu Leu Phe Val Met Val Ala Gly Phe Val Lys Gly Ser
 180 185 190

<210> 67
 <211> 719
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (500)..(714)
 <223> N = A, C, G, OR T/U

<400> 67
 ggatcctggt gcaagggcaa aaaaaaaca caacacaaga aggaataagt cctgaattat 60
 tggcttcac acatccacct tctccacccc aaaatggcac aaaagaaaca gttaccacac 120
 cctgcagacc ttttggtgta aaagagatga tgatgaactg ggggtgggaac aggtcatgaa 180
 gatctgtcta aaaaagtccc attcaggtga gtttgtacac accatcaagc agcgagcctc 240
 tcatcaatta ggggttaggga accaagggtc gattctcagg aaatcacaat ttcattcatt 300
 tactcaatat gaatttacaa agtgcctaca tattatccgc ttccacttgc agccatttct 360
 agataaaaaa gaaacctggc atctcaaagg ggccaccaag ttctccccga gtctaccact 420
 gaaaggacct tttttggaaa taggtttctt ctgtacctct ggaagggtaa catcttaaag 480
 ctgaatcaac tttaacctgn agggctaaca tatttagcaa tacttgcatc ccagacatac 540
 aacattaaaa gataactaa attctgaagg tagctatgct gcaaaatagt tttaaaatta 600
 aacaattgta cagtattcat ttatgcttgg aaattccagt cctagaccaa gcttggtggcc 660

accancattg accgttcttg ccatccagaa gagctgacag tgtcagttta atancctgg 719

<210> 68
 <211> 227
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (2)..(67)
 <223> XAA = ANYTHING

<400> 68
 Arg Xaa Leu Asn His Cys Gln Leu Phe Trp Met Ala Arg Thr Val Asn
 1 5 10 15
 Xaa Gly Gly His Lys Leu Gly Leu Gly Leu Glu Phe Pro Ser Ile Asn
 20 25 30
 Glu Tyr Cys Thr Ile Val Phe Asn Tyr Phe Ala Ala Leu Pro Ser Glu
 35 40 45
 Phe Ser Val Ser Phe Asn Val Val Cys Leu Gly Cys Lys Tyr Cys Ile
 50 55 60
 Cys Pro Xaa Arg Leu Lys Leu Ile Gln Leu Asp Val Thr Leu Pro Glu
 65 70 75 80
 Val Gln Lys Lys Pro Ile Ser Lys Lys Gly Pro Phe Ser Gly Arg Leu
 85 90 95
 Gly Glu Asn Leu Val Ala Pro Leu Arg Cys Gln Val Ser Phe Leu Ser
 100 105 110
 Arg Asn Gly Cys Lys Trp Lys Arg Ile Ile Cys Arg His Phe Val Asn
 115 120 125
 Ser Tyr Val Asn Glu Asn Cys Asp Phe Leu Arg Ile Glu Pro Trp Phe
 130 135 140
 Pro Asn Pro Asn Glu Ala Arg Cys Leu Met Val Cys Thr Asn Ser Pro
 145 150 155 160
 Glu Trp Asp Phe Phe Arg Gln Ile Phe Met Thr Cys Ser His Pro Ser
 165 170 175
 Ser Ser Ser Ser Leu Leu His Gln Lys Val Cys Arg Val Trp Leu Phe
 180 185 190
 Leu Leu Cys His Phe Gly Val Glu Lys Val Asp Val Met Lys Pro Ile
 195 200 205
 Ile Gln Asp Leu Phe Leu Leu Val Leu Cys Phe Phe Phe Ala Leu Ala
 210 215 220

Pro Gly Ser
225

<210> 69
<211> 311
<212> DNA
<213> Homo sapiens

<400> 69
ggatccgagg tacgcccgcc cgtgctcgcg cgtcagcgac gcgatgtcct cgcgcattctc 60
gttgatgacc gggagcagaa actgctcgaa atcctcctcg ggctccagca cctccacttc 120
ctccggttcc gccagctcga cgatgtccag gggccgcac tcttcccact gcctcggaac 180
cgcaatagcg atgtctgttg gagagagaaa accgacactc gctatgctta gcaatagaga 240
gcccgaatat tctgaaaac ttttaccctt tttcaacttt tcttctcaga ggtcgacgcg 300
gccggaatt c 311

<210> 70
<211> 102
<212> PRT
<213> Homo sapiens

<400> 70
Ile Arg Gly Arg Val Asp Leu Glu Glu Lys Leu Lys Lys Gly Lys Ser
1 5 10 15
Phe Gln Glu Tyr Ser Gly Ser Leu Leu Leu Ser Ile Ala Ser Val Gly
20 25 30
Phe Leu Ser Pro Thr Asp Ile Ala Ile Ala Val Pro Arg Gln Trp Glu
35 40 45
Glu Met Arg Pro Leu Asp Ile Val Glu Leu Ala Glu Pro Glu Glu Val
50 55 60
Glu Val Leu Glu Pro Glu Glu Asp Phe Glu Gln Phe Leu Leu Pro Val
65 70 75 80
Ile Asn Glu Met Arg Glu Asp Ile Ala Ser Leu Thr Arg Glu His Gly
85 90 95
Arg Ala Tyr Arg Gly Ser
100

<210> 71
<211> 501
<212> DNA
<213> Homo sapiens

<400> 71
ggatccggtg ctgccaatta aaaaaaaaaac tgtaaattcat cttaccaccc aaaagtgata 60
tggaactg tttgaatctg agcatggaca tgggtgtagt catcttttg aattataagt 120

gaaagtgata ggtaactcct tgtgttccat ttctcagagt agattgctat atccaaatga 180
 tcatgaacac cctcccatc ccacactcag atggaaagca gccagaaccc ctgccactgg 240
 attcttcagc acccttggga cagtctccaa ctgacacttc ccagcagggg aggagggcag 300
 gcacctttgg tgactcttca gtgagactcc atcgacattc agaatcttaa aatgttggtg 360
 atgaaaacca tggacctcca agtcattcctt accaaccctta aatgtagtgt tgtgacatcc 420
 aacgaaggac ttccacgtca cgtgggaata aatttgaaca gatacatcca attgaacata 480
 ggtcgacgcg gccgcgaatt c 501

<210> 72
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 72
 Glu Phe Ala Ala Ala Ser Thr Tyr Val Gln Leu Asp Val Ser Val Gln
 1 5 10 15
 Ile Tyr Ser His Val Thr Trp Lys Ser Phe Val Gly Cys His Asn Thr
 20 25 30
 Thr Phe Lys Val Gly Lys Asp Asp Leu Glu Val His Gly Phe His Tyr
 35 40 45
 Gln His Phe Lys Ile Leu Asn Val Asp Gly Val Ser Leu Lys Ser His
 50 55 60
 Gln Arg Cys Leu Pro Ser Ser Pro Ala Gly Lys Cys Gln Leu Glu Thr
 65 70 75 80
 Val Pro Arg Val Leu Lys Asn Pro Val Ala Gly Val Leu Ala Ala Phe
 85 90 95
 His Leu Ser Val Gly Trp Glu Gly Cys Ser Ser Phe Gly Tyr Ser Asn
 100 105 110
 Leu Leu Glu Met Glu His Lys Glu Leu Pro Ile Thr Phe Thr Tyr Asn
 115 120 125
 Ser Lys Arg Leu Gln Pro Cys Pro Cys Ser Asp Ser Asn Ser Phe Pro
 130 135 140
 Tyr His Phe Trp Val Val Arg Phe Thr Val Phe Phe Leu Ile Gly Ser
 145 150 155 160
 Thr Gly Ser

<210> 73
 <211> 747
 <212> DNA
 <213> Homo sapiens

<400> 73

ggatcctgtt gcttcaaaag tcaattttat agaatcccaa ggtgtctgtt ctttggatat 60
 gagtcggaaa tgaggaggat ttcttggaga aacttctggg gcaggaagat accagttttt 120
 cctgatcaga aagtgcacnt ggaagatacc aaggaaaacc acaaagaggt gcattctcct 180
 cacagtgagc tcggatacta tcattgatct caggaatgtg aggggttatg tgagaaattc 240
 cagtataatc aaaccattg atccatattc cagagtcccg tttaactgca tttccttcca 300
 agtcatggaa tgttctagtc atatgctgaa gaaacactct ctttggcttc ggattagcag 360
 gattggagct atatggaaaa aatgttccac tgcaaacaag gaggaatgta attgcacata 420
 ccaaagttaa agttagcatg gttttttttg tgctcttggc aaggtagatg aagttaatca 480
 tgtaataaaa tcttttcgca agagtatgta taagtattat tttggctaca gttgcagttc 540
 catacagaca aacggagacc atagaagtgg ttataccatg agagagactg tccaataaga 600
 gagatgaaca ctgctataat gagaacggta acaaggctag tgaaccagct gatcaaagtg 660
 atgccaagtc cacacaagaa gtccttcttg tagttaccag tcttatgttt gggctgcaaa 720
 aattttttgc ccaggtaaca aacaaca 747

<210> 74
 <211> 238
 <212> PRT
 <213> Homo sapiens

<400> 74
 Cys Cys Phe Val Pro Gly Gln Lys Ile Phe Ala Ala Gln Thr Asp Trp
 1 5 10 15
 Leu Gln Glu Gly Leu Leu Val Trp Thr Trp His His Phe Asp Gln Leu
 20 25 30
 Val His Pro Cys Tyr Arg Ser His Tyr Ser Ser Val His Leu Ser Tyr
 35 40 45
 Trp Thr Val Ser Leu Met Val Pro Leu Leu Trp Ser Pro Phe Val Cys
 50 55 60
 Met Glu Leu Gln Leu Pro Lys Tyr Leu Tyr Ile Leu Leu Arg Lys Asp
 65 70 75 80
 Phe Ile Thr Leu Thr Ser Ser Thr Leu Pro Arg Ala Gln Lys Lys Pro
 85 90 95
 Cys Leu Leu Trp Tyr Val Gln Leu His Ser Ser Leu Phe Ala Val Glu
 100 105 110
 His Phe Phe His Ile Ala Pro Ile Leu Leu Ile Arg Ser Gln Arg Glu
 115 120 125
 Cys Phe Phe Ser Ile Leu Glu His Ser Met Thr Trp Lys Glu Met Gln
 130 135 140
 Leu Asn Gly Thr Leu Glu Tyr Gly Ser Met Gly Leu Ile Ile Leu Glu
 145 150 155 160
 Phe Leu Thr Pro Leu Thr Phe Leu Arg Ser Met Ile Val Ser Glu Leu
 165 170 175
 Thr Val Arg Arg Met His Leu Phe Val Val Phe Leu Gly Ile Phe Xaa

180 185 190

Val His Phe Leu Ile Arg Lys Asn Trp Tyr Leu Pro Ala Pro Glu Val
 195 200 205

Ser Pro Arg Asn Pro Pro His Phe Arg Leu Ile Ser Lys Glu Gln Thr
 210 215 220

Pro Trp Asp Ser Ile Lys Leu Thr Phe Glu Ala Thr Gly Ser
 225 230 235

<210> 75
 <211> 712
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (712)
 <223> N = A, C G OR T/U

<400> 75
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 tctactatgt atacagcagt cttgaataaa ctgcaaacat gtaacaacag ttataatttg 120
 aaagagtctt ccaaatgtga acattctggc ctagaaccct tcccatctcc atcaaccag 180
 aagacatcaa attttcagaa gacaatcttt cctaggactt gtaaaacaaa atgtacaaaa 240
 tatattagtt tactaactct acttttgtca tacctggca acctctttaa catccagaaa 300
 gactagatgt tgtcaattag gactcgtctg tcttttatgt aactatata cacagataag 360
 taaaacaaaa tgcacagaca taatgattca tcttgctcg ctgtaaacag gatggcatag 420
 agctctctgc acctccccct cctctctcct cccctgaacc actgcacaaa cacaatgagt 480
 attactcaac aggtgatttg gccattcccc cccaaaaata tttcctatga attgtaacaa 540
 aaaggtattt acaaaatgtg attttgctac ctctaatttt aacatatcag gcacttcaga 600
 acatctaaaa agaagagaca tttcaaaaaa gcttagcatt gtcaactata tacacagtag 660
 tgaggaataa aatgcacaca aaacaatgga tagaatatga aaatgtcttc tn 712

<210> 76
 <211> 227
 <212> PRT
 <213> Homo sapiens

<400> 76
 Arg Arg His Phe His Ile Leu Ser Ile Val Leu Cys Ala Phe Tyr Ser
 1 5 10 15

Ser Leu Leu Cys Ile Leu Thr Met Leu Ser Phe Phe Glu Met Ser Leu
 20 25 30

Leu Phe Arg Cys Ser Glu Val Pro Asp Met Leu Lys Leu Glu Val Ala
 35 40 45

Lys Ser His Phe Val Asn Thr Phe Leu Leu Gln Phe Ile Gly Asn Ile
 50 55 60

Phe Gly Gly Glu Trp Pro Asn His Leu Leu Ser Asn Thr His Cys Val
65 70 75 80

Cys Ala Val Val Gln Gly Arg Arg Glu Glu Gly Glu Val Gln Arg Ala
85 90 95

Leu Cys His Pro Val Tyr Ser Glu Ala Arg Ile Ile Met Ser Val His
100 105 110

Phe Val Leu Leu Ile Cys Val Tyr Ser Val His Lys Gly Gln Thr Ser
115 120 125

Pro Asn Gln His Leu Val Phe Leu Asp Val Lys Glu Val Ala Ser Val
130 135 140

Gln Lys Ser Thr Asn Ile Phe Cys Thr Phe Cys Phe Thr Ser Pro Arg
145 150 155 160

Lys Asp Cys Leu Leu Lys Ile Cys Leu Leu Gly Trp Arg Trp Glu Gly
165 170 175

Phe Ala Arg Met Phe Thr Phe Gly Arg Leu Phe Gln Ile Ile Thr Val
180 185 190

Val Thr Cys Leu Gln Phe Ile Gln Asp Cys Cys Ile His Ser Arg Gln
195 200 205

Ile Asn Ser Leu Leu Glu Thr Ser Ser Leu Ser Arg Cys Leu Glu Val
210 215 220

Pro Gly Ser
225

<210> 77

<211> 605

<212> DNA

<213> Homo sapiens

<400> 77

ggatccctgc caaagggttta aaggtatgtc cgccatgcat tcctcccca agtgacact 60
gatggcagat acacttctta caagtccagc aaaatacact aagtttttca tgggtgatttt 120
cacatttgct cttttcattt tcttcatgtt tggtgagact gcagagttga agagtatcaa 180
gctgttgtgt tacttcttct gcccaacgac aatttactag ttctcgtagc tggagtggag 240
cacggcaatg aggacattga gctctctgct ctgtcagcca gcgcctaata cagctgaaac 300
aacacagttt ggagcaatga ggacacaggc gtgcatcccg caatttctcc atacaaatga 360
aacatcgga aacctcagca atgctctcca cgctctgttc atccattgcc tccggctctc 420
ggcggggccg ctggcgaccc gcaggctccg cagtctgacc tcttaggcgc cggcccaggg 480
tcgccagatc aaatcgccga taaaagcccg gcgcccacgt cagggggctc tgacaaccgc 540
cccacctgcg cgccccatct cttcaggtcc agcgccgctt accccgtcga cgcggccgcg 600
aattc 605

<210> 78

<211> 195

<212> PRT
<213> Homo sapiens

<400> 78
Ile Arg Gly Arg Val Asp Gly Val Gly Gly Ala Gly Pro Glu Glu Met
1 5 10 15
Gly Arg Ala Gly Gly Ala Val Val Arg Ala Pro Arg Gly Arg Arg Ala
20 25 30
Phe Ile Gly Asp Leu Ile Trp Arg Pro Arg Ala Gly Ala Glu Val Arg
35 40 45
Leu Arg Ser Leu Arg Val Ala Ser Gly Pro Ala Glu Ser Arg Arg Gln
50 55 60
Trp Met Asn Arg Ala Trp Arg Ala Leu Leu Arg Phe Ser Asp Val Ser
65 70 75 80
Phe Val Trp Arg Asn Cys Gly Met His Ala Cys Val Leu Ile Ala Pro
85 90 95
Asn Cys Val Val Ser Ala Val Leu Gly Ala Gly Gln Ser Arg Glu Leu
100 105 110
Asn Val Leu Ile Ala Val Leu His Ser Ser Tyr Glu Asn Ile Val Val
115 120 125
Gly Gln Lys Lys His Asn Ser Leu Ile Leu Phe Asn Ser Ala Val Ser
130 135 140
Pro Asn Met Lys Lys Met Lys Arg Thr Asn Val Lys Ile Thr Met Lys
145 150 155 160
Asn Leu Val Tyr Phe Ala Gly Leu Val Arg Ser Val Ser Ala Ile Ser
165 170 175
Val His Phe Gly Glu Glu Cys Met Ala Asp Ile Pro Leu Asn Leu Trp
180 185 190
Gln Gly Ser
195

<210> 79
<211> 875
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (569)..(875)
<223> N = A, C, G OR T/U

<400> 79

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ggatccatta cctttgaaag agccaaaaaa caaaaaaaa aaaaaaaaaa aattaccatg 60
ccagttttat tcccgttgaa tatttacacc ttggacagca aaccttgctc acataaagta 120
gaaaacagat acaataaaac atggccttgaa aaatgaccag agtatgcacc ttagtagtactg 180
tacactaaat aaaatacaca aggcagcaat acttaggggc cagaaacact gcttactaca 240
agtcagttac ggaatcataa tttacagtaa aaatgggcac gtcccaaggc tcaatttttc 300
tttttctttt gtcatttaca gtagaataaa tattttgttg ctattgctac actttaattt 360
acatttctaac ctattaaatg cagaaagcta gtgtaaagca tatagattaa gtgtaggtcc 420
catacgtatg acagtttgtt caagactagt aggtttttgt ttttgtatct ttttttaact 480
tattaaatgg ctagtgggaa agatttgtgc ttgtgatcag ctcttaactt caattttaca 540
tcaaaacgtc cctgaaaacg gtctttctna ctggacccaa tgttctcacc gtacgcctta 600
cactntatgc gaattcagtg tccatggtaa gatgggtgaa tgtacggccg caaggggctt 660
naagtanttg gcttgaagga attgcctagt ccggaaatct gcaaggaaac cagggggagt 720
gccagtccaa atctcccatt ccacttatct tacttattnn ttgccgtgac tgacggaagg 780
ctttgggtna cttatcntgg gaagntccag gctattttgg agctagttga nctaactggt 840
gnctttaaaa gccggttgcc tttgaccaa attan 875

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<210> 80
<211> 276
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (11)..(65)
<223> XAA = ANYTHING

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<400> 80
Asn Phe Gly Gln Arg Gln Pro Ala Phe Lys Xaa Thr Ser Xaa Asn Leu
  1              5              10              15

Gln Asn Ser Leu Xaa Leu Pro Xaa Ile Ser Xaa Pro Lys Pro Ser Val
      20              25              30

Ser His Gly Xaa Xaa Val Arg Val Glu Trp Glu Ile Trp Thr Gly Asn
      35              40              45

Ser Pro Gly Phe Leu Ala Asp Phe Arg Thr Arg Gln Phe Leu Gln Ala
      50              55              60

Xaa Tyr Xaa Lys Pro Leu Ala Ala Val His Ser Pro Ile Leu Pro Trp
      65              70              75              80

Thr Leu Asn Ser His Xaa Val Gly Val Arg Glu His Trp Val Gln Xaa
      85              90              95

Glu Arg Pro Phe Ser Gly Thr Phe Cys Lys Ile Glu Val Lys Ser Ser
      100              105              110

Gln Ala Gln Ile Phe Pro Thr Ser His Leu Ile Ser Lys Lys Ile Gln
      115              120              125

Lys Gln Lys Pro Thr Ser Leu Glu Gln Thr Val Ile Arg Met Gly Pro
      130              135              140

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Thr Leu Asn Leu Tyr Ala Leu His Leu Ser Ala Phe Asn Arg Leu Glu
145 150 155 160

Cys Lys Leu Lys Cys Ser Asn Ser Asn Lys Ile Phe Ile Leu Leu Met
165 170 175

Thr Lys Glu Lys Glu Lys Leu Ser Leu Gly Thr Cys Pro Phe Leu Leu
180 185 190

Ile Met Ile Pro Leu Thr Cys Ser Lys Gln Cys Phe Trp Pro Leu Ser
195 200 205

Ile Ala Ala Leu Cys Ile Leu Phe Ser Val Gln Tyr Tyr Arg Cys Ile
210 215 220

Leu Trp Ser Phe Phe Lys Pro Cys Phe Ile Val Ser Val Phe Tyr Phe
225 230 235 240

Met Ala Arg Phe Ala Val Gln Gly Val Asn Ile Gln Arg Glu Asn Trp
245 250 255

His Gly Asn Phe Phe Phe Phe Phe Phe Leu Phe Phe Gly Ser Phe Lys
260 265 270

Gly Asn Gly Ser
275

<210> 81
<211> 631
<212> DNA
<213> Homo sapiens

<400> 81
ggatccctcc acctcgatct tgccgcagtc tgcgatgac acatccttca ggggtttatc 60
ccggtgtgtc gtcttgggtc tctccacctt ccgcaccacc tccatgccct ctagaacttt 120
gccaaacacc acatgcttgc catctagcca ggctgtcttg actgtcgtga tgaagaactg 180
ggagccgttg gtgtctttgc ctgcgttggc catgctcacc cagccaggcc cgtagtgctt 240
cagtttgaag ttctcatcgg ggaagcgctc accgtagatg ctctttcctc ctgtgccatc 300
tcccctgggtg aagtctccgc cctggatcat gaagtccttg attacacgat ggaatttgc 360
gtttttgtag ccaaactcctt tctctcctgt agctaaggcc acaaaattat ccactgtttt 420
tggaacagtc tttccgaaga gaccaaagat caccggccct acatcttcat ctccaattcg 480
taggtcaaaa tacaccttga cggtgacttt gggcccttct ttcttctcat cggccgcaga 540
aggtcccggc agcagcagga agaagacgga ccccgcatg aaggcggcgg caaggagcac 600
ccttatgttg cgtcgacgcg gccgcgaatt c 631

<210> 82
<211> 210
<212> PRT
<213> Homo sapiens

<400> 82
Asn Ser Arg Pro Arg Arg Asn Ile Arg Val Leu Leu Ala Ala Ala
1 5 10 15

Phe Ile Ala Gly Ser Val Phe Phe Leu Leu Leu Pro Gly Pro Ser Ala
20 25 30

Ala Asp Glu Lys Lys Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe
35 40 45

Asp Leu Arg Ile Gly Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu
50 55 60

Phe Gly Lys Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala
65 70 75 80

Thr Gly Glu Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val
85 90 95

Ile Lys Asp Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly
100 105 110

Thr Gly Gly Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe
115 120 125

Lys Leu Lys His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly
130 135 140

Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala
145 150 155 160

Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met
165 170 175

Glu Val Val Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys
180 185 190

Pro Leu Lys Asp Val Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu
195 200 205

Gly Ser
210

<210> 83
<211> 452
<212> DNA
<213> Homo sapiens

<400> 83
ggatccgccc attgtaattc catgaataag tgcaacataa ggtttctggc aagaacctga 60
aagaacaga gcaacagcat tattcagcat atattcttct ctgaagaaaa ctggagctat 120
cttctgtttt gccttttccag cttccgagat cactaggaag gaaagattac aaataaaaaa 180
aaaaagattt aatagtcaac attgtcaact agatcaaaaag tattatgaaa attaaatact 240
gggggaaggg agtactctaa aatgacttgt taaaagtttt gaagttgccc ctgccacaga 300
cattatatta tagtcacaga tccatagtcc aatgtcaaaag cttcaaggca aaaattccta 360
ttcttgtttt ccatgtttct tacaatatgt tagattagaa attataggct gggcatggtg 420
gctcaaacct gtgtcgacgc ggccgcgaat tc 452

<210> 84
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 84
 Ile Arg Gly Arg Val Asp Thr Gly Leu Ser His His Ala Gln Pro Ile
 1 5 10 15
 Ile Ser Asn Leu Thr Phe Cys Lys Lys His Gly Lys Gln Glu Glu Phe
 20 25 30
 Leu Pro Ser Phe Asp Ile Gly Leu Trp Ile Cys Asp Tyr Asn Ile Met
 35 40 45
 Ser Val Ala Gly Ala Thr Ser Lys Leu Leu Thr Ser His Phe Arg Val
 50 55 60
 Leu Pro Ser Pro Ser Ile Phe Ser Tyr Phe Ser Ser Gln Cys Leu Leu
 65 70 75 80
 Asn Leu Phe Phe Phe Ile Cys Asn Leu Ser Phe Leu Val Ile Ser Glu
 85 90 95
 Ala Glu Lys Ala Lys Gln Lys Ile Ala Pro Val Phe Phe Arg Glu Glu
 100 105 110
 Tyr Met Leu Asn Asn Ala Val Ala Leu Phe Leu Ser Gly Ser Cys Gln
 115 120 125
 Lys Pro Tyr Val Ala Leu Ile His Gly Ile Thr Met Gly Gly Ser
 130 135 140

<210> 85
 <211> 752
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (462)..(748)
 <223> N = A, C, G OR T/U

<400> 85
 ggatccggtc aggggaaaga agggccggtg ctggatctgg cagtaccaga gcagcagcaa 60
 cagcaggagc agcaggggca gcagcaggct gccgatttcc agcccggagg ggccggggtc 120
 ggaccccggc gggcaggggg gatttggggg accgactctc gtggacacgt ggcagtggag 180
 aacgcagttg ggagggaggt gaaggctgcc caggggtctg gtgtcgtcgc ctagcagctg 240
 cccttggtag atgagtcgca cctgctgttc ccggccggga aactgggtcc ttttcaagga 300
 gccaatggtg tcgtggggcc aggccttggc cacctgctct gaatcattga ggaatttcag 360
 cccgtagcac gaggggctcc tgcggggagt ccggggctgg cgggtgttgc gtgaaccccg 420
 tgctgggctc tggctgtgca gcttgacctt ctggtgtctc angctggggg tctctgcccc 480

tggggccttc cctctcatgc tgtcggtagc tgccatggct tgccgctggg ctgggatggc 540
 gttgggggtcc ctgacggctg gggcaatggg tccccggcct tnacgggtgtg ccttgaaaac 600
 ccagccangg ccaacaccag aanggaagg caagcncga naaaaggacg gtcacttcat 660
 caccacaacc nttnatcang gtcatngcgc ctggcttgcc cgccggcnta ccgancgccg 720
 ggttcccan ttccttnacc cggccggnaa tt 752

<210> 86
 <211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(94)
 <223> XAA = ANYTHING

<400> 86
 Xaa Pro Ala Gly Xaa Arg Xaa Trp Gly Thr Arg Arg Ser Val Xaa Arg
 1 5 10 15
 Arg Ala Ser Gln Ala Xaa Pro Xaa Xaa Gly Trp Val Met Lys Pro Ser
 20 25 30
 Phe Xaa Arg Xaa Leu Pro Cys Xaa Ser Gly Val Gly Xaa Gly Trp Val
 35 40 45
 Phe Lys Ala His Arg Xaa Gly Arg Gly Pro Ile Ala Pro Ala Val Arg
 50 55 60
 Asp Pro Asn Ala Ile Pro Ala Gln Arg Gln Ala Met Ala Ala Thr Asp
 65 70 75 80
 Ser Met Arg Gly Lys Ala Pro Gly Ala Glu Thr Pro Ser Xaa Arg His
 85 90 95
 Gln Lys Val Lys Leu His Ser Gln Ser Pro Ala Arg Gly Ser Gln Gln
 100 105 110
 His Arg Gln Pro Arg Thr Pro Arg Arg Ser Pro Ser Cys Tyr Gly Leu
 115 120 125
 Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp Pro His Asp
 130 135 140
 Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly Arg Glu Gln Gln
 145 150 155 160
 Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly Asp Asp Thr Gln Thr
 165 170 175
 Leu Gly Ser Leu His Leu Pro Pro Asn Cys Val Leu His Cys His Val
 180 185 190
 Ser Thr Arg Val Gly Pro Pro Asn Pro Pro Cys Pro Pro Gly Ser Glu

195 200 205

Pro Gly Pro Ser Gly Leu Glu Ile Gly Ser Leu Leu Leu Pro Leu Leu
 210 215 220

Leu Leu Leu Leu Leu Leu Leu Trp Tyr Cys Gln Ile Gln Tyr Arg Pro
 225 230 235 240

Phe Phe Pro Leu Thr Gly Ser
 245

<210> 87
 <211> 396
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (375)..(395)
 <223> N = A, C, G OR T/U

<400> 87
 ggatcccaga gtattctgac agataaaatc ggggaggcag ttatgaatac cactctcaca 60
 ctctgcaata tctttgcagc tattgtcctc tgtgagctca tagccagtcc cgcagctgct 120
 gtcccgtctg cagcggaag agcccactgt gttgatgcag gattctccaa gccggcagct 180
 gtggctgccc gtgatgcatt cattgacatc ttcacaggag acaccatcag acagcagctg 240
 gtagccacag aagcaggagc agaccacctc gtcacccgtg tctcggcact gctgcttgca 300
 gggcccgct cctcggcagc ggtcattcag atatgggtcc tcttgttcct cctcaacctc 360
 aatgatctta tccgnnnttg gangccccc acntnc 396

<210> 88
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(8)
 <223> XAA = ANYTHING

<400> 88
 Xaa Xaa Xaa Gly Xaa Pro Xaa Xaa Asp Lys Ile Ile Glu Val Glu Glu
 1 5 10 15

Glu Gln Glu Asp Pro Tyr Leu Asn Asp Arg Cys Arg Gly Gly Gly Pro
 20 25 30

Cys Lys Gln Gln Cys Arg Asp Thr Gly Asp Glu Val Val Cys Ser Cys
 35 40 45

Phe Val Gly Tyr Gln Leu Leu Ser Asp Gly Val Ser Cys Glu Asp Val
 50 55 60

Asn Glu Cys Ile Thr Gly Ser His Ser Cys Arg Leu Gly Glu Ser Cys
65 70 75 80

Ile Asn Thr Val Gly Ser Phe Arg Cys Gln Arg Asp Ser Ser Cys Gly
85 90 95

Thr Gly Tyr Glu Leu Thr Glu Asp Asn Ser Cys Lys Asp Ile Asp Glu
100 105 110

Cys Glu Ser Gly Ile His Asn Cys Leu Pro Asp Phe Ile Cys Gln Asn
115 120 125

Thr Leu Gly Ser
130

<210> 89
<211> 558
<212> DNA
<213> Homo sapiens

<400> 89
ggatccagac ccacgagggg catatgaatt ttcattcagc agcttgatgg tgctgggtgaa 60
gtctgtgctg tccagtttct cgcacaactt tctcttcagg tcatcccaat ataagcgacg 120
tgctgcaggg aagtcctctc ctggctcctc cctcactgga gactcgggtc ctgccagtct 180
ctcacactca gtttttggtt ctaccccttt acaatagccc aagtagccaa tcataaatcc 240
aatcaagaaa aagacgatca cagcaatagt cccatagcag atacttccac tacacctttt 300
tggntttgtg acattggcct ttgtgttatt gtcagcattt tcttcttcat ctacagcaag 360
tttcatctnc acatgactgt tctgccatc tacttgccga gccaggctga accgggtata 420
tgacaatggt tctccaccaa acaagttaga gaatgctgat ctagcttgat ccatcattct 480
gaactgccac acagaagaca ctagecgcgc ctncgtcccg agccgcaccc gatatcccgt 540
cgacgcggcc gcgaattc 558

<210> 90
<211> 186
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (16)..(85)
<223> XAA = ANYTHING

<400> 90
Glu Phe Ala Ala Ala Ser Thr Gly Tyr Arg Val Arg Leu Gly Thr Xaa
1 5 10 15

Asp Ala Leu Val Ser Ser Val Trp Gln Phe Arg Met Met Asp Gln Ala
20 25 30

Arg Ser Ala Phe Ser Asn Leu Phe Gly Gly Glu Pro Leu Ser Tyr Thr
35 40 45

Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp Asn Ser His Val Xaa

50 55 60

Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala Asp Asn Asn Thr Lys
65 70 75 80

Ala Asn Val Thr Xaa Pro Lys Arg Cys Ser Gly Ser Ile Cys Tyr Gly
85 90 95

Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly Phe Met Ile Gly Tyr
100 105 110

Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr Glu Cys Glu Arg Leu
115 120 125

Ala Gly Thr Glu Ser Pro Val Arg Glu Glu Pro Gly Glu Asp Phe Pro
130 135 140

Ala Ala Arg Arg Leu Tyr Trp Asp Asp Leu Lys Arg Lys Leu Ser Glu
145 150 155 160

Lys Leu Asp Ser Thr Asp Phe Thr Ser Thr Ile Lys Leu Leu Asn Glu
165 170 175

Asn Ser Tyr Val Pro Arg Gly Ser Gly Ser
180 185

<210> 91
<211> 461
<212> DNA
<213> Homo sapiens

<400> 91
ggatcccttt gtatataaaa tgggtgaaagc tgacttgaat gtgccgtcac cactctgctg 60
ggaaaaacag atgaagggtgg ccagagagaaa accacagact ccagcgtaag ctgttctcca 120
ttgaacagga acaaggctga agttgggtcag ctgtacaaag ggccagtaca tcagtccact 180
cagataggta ttccagaatt tctgtttcag gtccaaaaat atgtcatcct ttccttgagg 240
aatgctcata ccgacataga aggccgagac cgcgatgggc gcaccgacca cctgggtcgca 300
cagcaacttg gccagcaggg cgtgcggcgc tcggcccggg agcgcgcgct ccagcaggcg 360
cagccacacg tagttgaagt tggcgtggaa ggtcaccacc aacgtggcca cgcgccgcgt 420
ctggcgccag ttggcctcgc ggtcgacgcg gccgcgaatt c 461

<210> 92
<211> 153
<212> PRT
<213> Homo sapiens

<400> 92
Ile Arg Gly Arg Val Asp Arg Glu Ala Asn Trp Arg Gln Thr Arg Arg
1 5 10 15
Val Ala Thr Leu Val Val Thr Phe His Ala Asn Phe Asn Tyr Val Trp
20 25 30

Leu Arg Leu Leu Glu Arg Ala Leu Pro Gly Arg Ala Pro His Ala Leu
 35 40 45
 Leu Ala Lys Leu Leu Cys Asp Gln Val Val Gly Ala Pro Ile Ala Val
 50 55 60
 Ser Ala Phe Tyr Val Gly Met Ser Ile Leu Gln Gly Lys Asp Asp Ile
 65 70 75 80
 Phe Leu Asp Leu Lys Gln Lys Phe Trp Asn Thr Tyr Leu Ser Gly Leu
 85 90 95
 Met Tyr Trp Pro Phe Val Gln Leu Thr Asn Phe Ser Leu Val Pro Val
 100 105 110
 Gln Trp Arg Thr Ala Tyr Ala Gly Val Cys Gly Phe Leu Trp Ala Thr
 115 120 125
 Phe Ile Cys Phe Ser Gln Gln Ser Gly Asp Gly Thr Phe Lys Ser Ala
 130 135 140
 Phe Thr Ile Leu Tyr Thr Lys Gly Ser
 145 150

<210> 93
 <211> 603
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> modified_base
 <222> (541)..(567)
 <223> N = A, C, G OR T/U

<400> 93
 ggatccagtg ctataataac nattacacac attgtaactc ctacacaatt tgaaattttc 60
 aagttaagac aaaggtaact atatatagaa gcagtatgtt ttctgaaccc ttacagattg 120
 ttttgcacac tcctggatta cacacatctc atcaatctca agaataaaat caaagtcttt 180
 ggcttgacag ccttccacaa tctgacctct gttttctcgc cagcctcatc tcctgtcatt 240
 cacaacattt ccagcattcc aaccagtctg aacttttgca gtttcccacg tgcgctaggc 300
 tctttcttca tcagcatctc tatgcatgct gtctcctgct actggaatgc cctcattctc 360
 gttgcttcct gttttgaaga aaagctgtga taccggcaac agtggtttaag tatcacacgg 420
 gtagttaaaa ggcaagttgg tcctatctga catgtggaaa tggccagctc gttagaaggc 480
 agtacctggt gaagcccggg cagcgcagtt cagccagcg acagtggaaa gcccttcct 540
 ngcaagcgcg cttccggcac tagccgnacc ccgncgagct ctggtcgacg cggccgcgaa 600
 ttc 603

<210> 94
 <211> 195
 <212> PRT
 <213> Homo sapiens

<220>

<221> MOD_RES
 <222> (13)
 <223> XAA = ANYTHING

<400> 94
 Glu Phe Ala Ala Ala Ser Thr Arg Ala Arg Arg Gly Xaa Ala Ser Ala
 1 5 10 15
 Gly Ser Ala Leu Ala Arg Glu Gly Leu Ser Thr Val Ala Gly Val Asn
 20 25 30
 Ser Arg Ala Arg Ala Ser Pro Gly Thr Ala Phe Arg Ala Gly His Phe
 35 40 45
 His Met Ser Asp Arg Thr Asn Leu Pro Phe Asn Tyr Pro Cys Asp Thr
 50 55 60
 Thr Leu Leu Pro Val Ser Gln Leu Phe Phe Lys Thr Gly Ser Asn Glu
 65 70 75 80
 Asn Glu Gly Ile Pro Val Ala Gly Asp Ser Met His Arg Asp Ala Asp
 85 90 95
 Glu Glu Arg Ala Arg Thr Trp Glu Thr Ala Lys Val Gln Thr Gly Trp
 100 105 110
 Asn Ala Gly Asn Val Val Asn Asp Arg Arg Gly Trp Arg Glu Asn Arg
 115 120 125
 Gly Gln Ile Val Glu Gly Cys Gln Ala Lys Asp Phe Asp Phe Ile Leu
 130 135 140
 Glu Ile Asp Glu Met Cys Val Ile Gln Glu Cys Ala Lys Gln Ser Val
 145 150 155 160
 Arg Val Gln Lys Thr Tyr Cys Phe Tyr Ile Leu Pro Leu Ser Leu Glu
 165 170 175
 Asn Phe Lys Leu Cys Arg Ser Tyr Asn Val Cys Asn Xaa Tyr Tyr Ser
 180 185 190
 Thr Gly Ser
 195

<210> 95
 <211> 813
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (529)..(779)
 <223> N = A, C, G OR T/U

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<400> 95
ggatcctact gaaatggaaa aggttgaaaa atgtatcagt gatgccatga gttggctgaa 60
tagtaagatg aatgcacaga acaaactaag tctcactcaa gatcctgtgg taaaagtttc 120
agaaatagta gcaaagtcaa aggaactgga taattttctgt aaccccatca tttacaagcc 180
caaaccaaaa gcagaagttc ctgaagacaa accaaaagct aatagtgaac acaatggccc 240
aatggatgga cagagtggaa ctgaaactaa atcagattca acaaaagaca gctcacagca 300
tactaaatcc tctggagaga tggaagtgga ctaagtctta attttacctt cacattaatt 360
caaaccgtgc aagtaaccac ggggtccatc ttttacatct ggtacacaca acagacgctc 420
agttgttctt aaccactttt gtcatttggt ttttgagta gttttgaaaa gtgggtttata 480
ttgagtgcac ttctggatcat ttccattgct gcttatatgc agtggtagnc cgaattagat 540
ttaccaggac aatctaagct ttccggataa ttttatatat caaacattcn ggatggatac 600
ctagttggca acagtctacc ttatttaagc ttctactggg ataaacctca ttnctttatt 660
caggaaagga tctttaatgn antattggtg naaaagccta gattaatngc tcttantttg 720
aaaaccaatg gaaaattgga ngggnttaaa gttccgaggc ctggcctttt ttagtatggg 780
atgntccant taaataaact caattttcct ctt 813

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<210> 96
<211> 258
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (8)..(70)
<223> XAA = ANYTHING

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<400> 96
Lys Arg Lys Ile Glu Phe Ile Xaa Xaa His Pro Ile Leu Lys Lys Ala
  1             5             10             15
Arg Pro Arg Asn Phe Xaa Pro Xaa Gln Phe Ser Ile Gly Phe Gln Xaa
          20             25             30
Lys Ser Xaa Ser Arg Leu Xaa His Gln Xaa Xaa Ile Lys Asp Pro Phe
          35             40             45
Leu Asn Lys Xaa Met Arg Phe Ile Pro Val Glu Ala Ile Arg Thr Val
          50             55             60
Ala Asn Val Ser Ile Xaa Asn Val Tyr Ile Lys Leu Ser Gly Lys Leu
          65             70             75             80
Arg Leu Ser Trp Ile Phe Gly Leu Pro Leu His Ile Ser Ser Asn Gly
          85             90             95
Asn Asp Gln Lys Cys Thr Gln Tyr Lys Pro Leu Phe Lys Thr Thr Pro
          100             105             110
Lys Thr Lys Gln Lys Trp Leu Arg Thr Thr Glu Arg Leu Leu Cys Val
          115             120             125
Pro Asp Val Lys Asp Gly Pro Arg Gly Tyr Leu His Gly Leu Asn Cys
          130             135             140

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Glu Gly Lys Ile Lys Thr Ser Thr Ser Ile Ser Pro Glu Asp Leu Val
145 150 155 160

Cys Cys Glu Leu Ser Phe Val Glu Ser Asp Leu Val Ser Val Pro Leu
165 170 175

Cys Pro Ser Ile Gly Pro Leu Cys Ser Leu Leu Ala Phe Gly Leu Ser
180 185 190

Ser Gly Thr Ser Ala Phe Gly Leu Gly Leu Met Met Gly Leu Gln Lys
195 200 205

Leu Ser Ser Ser Phe Asp Phe Ala Thr Ile Ser Glu Thr Phe Thr Thr
210 215 220

Gly Ser Val Arg Leu Ser Leu Phe Cys Ala Phe Ile Leu Leu Phe Ser
225 230 235 240

Gln Leu Met Ala Ser Leu Ile His Phe Ser Thr Phe Ser Ile Ser Val
245 250 255

Gly Ser

<210> 97
<211> 478
<212> DNA
<213> Homo sapiens

<400> 97
ggatccgggg tcgaagcagt tggattccat gatgggaagg ccattggcct ctcggtattt 60
cacaagcctc tcagcttcgc ggcgggacca ctctttcatc ctgtagtcag gcagataggc 120
cacaaagggtg ctgccaaagg ccaggatgat ggagacgcca aagaagaaga caagtcgcat 180
gttccagacg tccaaaacgg ggtccttgtc ataaccatgg gagtctgggt tcttctcata 240
caagttttcg tctcggggtt ctgggtcctc ttgccacggt gtggtcgggt ctggggggccg 300
ctttcccgcc acagcggacg gggcgaccac agtctggag aagctagatt cccagcggac 360
gcggggcgcc gggagccctc gcgtcgccgc tgccgcaaaa agacggcgag cgctcaaacc 420
aaacagccca gccgccatga cagatggtgc ttgcaggggt cgacgcggcc gcgaattc 478

<210> 98
<211> 159
<212> PRT
<213> Homo sapiens

<400> 98
Asn Ser Arg Pro Arg Arg Pro Leu Gln Ala Pro Ser Val Met Ala Ala
1 5 10 15
Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala Ala Thr
20 25 30
Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser Phe Ser Arg
35 40 45

Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro Pro Glu Pro
50 55 60

Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu Asn Leu Tyr
65 70 75 80

Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro Val Leu Asp
85 90 95

Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser Ile Ile Leu
100 105 110

Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr Arg Met Lys
115 120 125

Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala
130 135 140

Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Gly Ser
145 150 155

<210> 99
<211> 258
<212> DNA
<213> Homo sapiens

<400> 99
ggatcctgag tagggcaata tctccaggca gaagtcccgga aatccaagc agcaggtgcc 60
aaggccagag cacgtcgggt ggcaggaaca tggcccgtcc agggcgccac agcgcattgga 120
gcagctctct tgggcatctg ctgtgggtcc ggggcccggg ccgagggctg tcgccagcag 180
cagcagggcc cagggcagga gggctggctt catggtgcag cctgtgtctg cagccagcgt 240
cgacgcggcc gccaattc 258

<210> 100
<211> 86
<212> PRT
<213> Homo sapiens

<400> 100
Glu Phe Ala Ala Ala Ser Thr Leu Ala Ala Asp Thr Gly Cys Thr Met
1 5 10 15

Lys Pro Ala Leu Leu Pro Trp Ala Leu Leu Leu Ala Thr Ala Leu
20 25 30

Gly Pro Gly Pro Gly Pro Thr Ala Asp Ala Gln Glu Ser Cys Ser Met
35 40 45

Arg Cys Gly Ala Leu Asp Gly Pro Cys Ser Cys His Pro Thr Cys Ser
50 55 60

Gly Leu Gly Thr Cys Cys Leu Asp Phe Arg Asp Phe Cys Leu Glu Ile

65

70

75

80

Leu Pro Tyr Ser Gly Ser
85

<210> 101

<211> 664

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (524)..(662)

<223> N = A, C, G OR T/U

<400> 101

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ggatccctga aagtgaaca gaaagtacag catctgcacc aaattctcca agaacaccgt 60
taacacctcc gctgtcttct ggtgcttcca gtaccacaga tgtttgcagt gtatttgatt 120
ccgatcattc gagccctttt cactcaagca atgataccgt ctttatccaa gttactctgc 180
cccatggccc aagatctgct tctgtatcat ctataagttt aaccaaaggc actgatgaag 240
tgcctgtccc tctcctgtt cctccacgaa gacgaccaga atctgcccc gcagaatctt 300
caccatctaa gattatgtct aagcatttgg acagtcccc agccattcct cctaggcaac 360
ccacatcaaa agcctattca ccacgatatt caatatcaga ccggacctct atctcagacc 420
ctcctgaaag ccctccctta ttaccaccac gaaggaaaaa aaacctggag cactgtgttc 480
taactacat cattccacct cccctttggg caaaaaggac atgnaatgct tntccaaca 540
ggccttgccc ttacaccact ctctnaacac tttctacgac aagangattg catacacatg 600
ccagaagggn ctcttcntgt ggcgctgtct cngaaagatt taattctact ctcaaactna 660
angg                                     664

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<210> 102

<211> 207

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (1)..(43)

<223> XAA = ANYTHING

<400> 102

Xaa Xaa Val Glu Asn Ile Phe Xaa Arg Gln Arg His Xaa Lys Xaa Pro
1 5 10 15

Phe Trp His Val Tyr Ala Ile Xaa Leu Ser Lys Val Xaa Arg Glu Trp
20 25 30

Cys Lys Gly Lys Ala Cys Trp Xaa Lys His Xaa Met Ser Phe Leu Pro
35 40 45

Lys Gly Glu Val Glu Trp Leu Glu His Ser Ala Pro Gly Phe Phe Ser
50 55 60

Phe Val Val Val Ile Arg Glu Gly Phe Gln Glu Gly Leu Arg Arg Ser

65	70	75	80
Gly Leu Ile Leu Asn Ile Val Val Asn Arg Leu Leu Met Trp Val Ala			
	85	90	95
Glu Glu Trp Leu Gly Asp Cys Pro Asn Ala Thr Ser Met Val Lys Ile			
	100	105	110
Leu Leu Gly Gln Ile Leu Val Val Phe Val Glu Glu Gln Glu Glu Gly			
	115	120	125
Gln Ala Leu His Gln Cys Leu Trp Leu Asn Leu Met Ile Gln Lys Gln			
	130	135	140
Ile Leu Gly His Gly Ala Glu Leu Gly Arg Arg Tyr His Cys Leu Ser			
	145	150	155
Glu Lys Gly Ser Asn Asp Arg Asn Gln Ile His Cys Lys His Leu Trp			
	165	170	175
Tyr Trp Lys His Gln Lys Gln Ala Glu Val Leu Thr Val Phe Leu Glu			
	180	185	190
Asn Leu Val Gln Met Leu Tyr Phe Leu Phe His Phe Gln Gly Ser			
	195	200	205

<210> 103
 <211> 762
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (464)..(746)
 <223> N = A, C, G OR T.U

<400> 103
 ggatcccact gcaagcccca ccaggcggta ggggaagaag caggaggcca ggaaggcagc 60
 ccagagcgcc acatacagct tctgtgtgat ctccggctgg acccacatga acaagttctt 120
 gatcttctcc aggatgtcag ccatcttccc gaaaagggtc tgggctttct gggcgacgtc 180
 cagcaccagc tggaacttct cagacacagt caggtcttcc tttggagggt ccacgggctc 240
 agacacttcg ggcacgatgc tccactgtat ccgccacccc ctggcgatga ggtaattgag 300
 ggataacctc agaattgcta gaaataagaa caatgggatg gccagccat gccacacggc 360
 attcatgtac acggtgaagg caatggcaga cgtgtagacg gagtaccagt cggataaggc 420
 agagaggttc ttcacaaagt tagtgaccgg cttttggggg gggnacgct tgaccgctat 480
 ttttagtaac ctgcggcgct caggggttcc tnttgtctcc acagtgtctc ctcggtgga 540
 accgggaagt ccttccacgt acttccccga accggttcgt aaaaccactt tttgcaggcc 600
 ccgaggacag gcccttggct tccggngct tntgnttcca ttgntggcc tgggccctgc 660
 cctttttggg ggcttgggtg annccatctg ctncctcggt tntgggcctt nancacctc 720
 ttggacnntt ttggttcaag ttncantccg gccggttggc cg 762

<210> 104
 <211> 253

<212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (6)..(99)
 <223> XAA = ANYTHING

<400> 104
 Arg Pro Thr Gly Arg Xaa Xaa Thr Thr Lys Xaa Val Gln Glu Gly Xaa
 1 5 10 15
 Xaa Gly Pro Xaa Pro Lys Xaa Gln Met Xaa Ser Thr Lys Pro Pro Lys
 20 25 30
 Arg Ala Gly Pro Arg Pro Xaa Asn Gly Xaa Xaa Ser Xaa Arg Lys Pro
 35 40 45
 Arg Ala Cys Pro Arg Gly Leu Gln Lys Val Val Leu Arg Thr Gly Ser
 50 55 60
 Gly Lys Tyr Val Glu Gly Leu Pro Gly Ser Ser Arg Gly Asp Thr Val
 65 70 75 80
 Glu Thr Xaa Gly Thr Pro Glu Arg Arg Arg Leu Leu Lys Ile Ala Val
 85 90 95
 Lys Arg Xaa Pro Pro Gln Lys Pro Val Thr Asn Phe Val Lys Asn Leu
 100 105 110
 Ser Ala Leu Ser Asp Trp Tyr Ser Val Tyr Thr Ser Ala Ile Ala Phe
 115 120 125
 Thr Val Tyr Met Asn Ala Val Trp His Gly Trp Ala Ile Pro Leu Phe
 130 135 140
 Leu Phe Leu Ala Ile Leu Arg Leu Ser Leu Asn Tyr Leu Ile Ala Arg
 145 150 155 160
 Gly Trp Arg Ile Gln Trp Ser Ile Val Pro Glu Val Ser Glu Pro Val
 165 170 175
 Glu Pro Pro Lys Glu Asp Leu Thr Val Ser Glu Lys Phe Gln Leu Val
 180 185 190
 Leu Asp Val Ala Gln Lys Ala Gln Asn Leu Phe Gly Lys Met Ala Asp
 195 200 205
 Ile Leu Glu Lys Ile Lys Asn Leu Phe Met Trp Val Gln Pro Glu Ile
 210 215 220
 Thr Gln Lys Leu Tyr Val Ala Leu Trp Ala Ala Phe Leu Ala Ser Cys
 225 230 235 240
 Phe Phe Pro Tyr Arg Leu Val Gly Leu Ala Val Gly Ser

<210> 105
 <211> 676
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (606)..(671)
 <223> N = A, C, G OR T/U

<400> 105
 ggatccaggc atgagttctg tcctttgaac tccatagtga ccccttttta ccttggtcca 60
 gatgaggaca ggtgtcggga ttccgatgac ctcacagctc aagtacacct gggcaccagt 120
 gacattccag atgtccttgg ggggcgtcac tatggaagga ccttgctcgc aggtgccctt 180
 gctgacctgg gtgatggcct tctccccgcg gctctcggcc ctctggctgg cggcgcgag 240
 ctggcagccg ctcgggtagg tgggtgccgc gctgcgcac accgggtagc ggctcttgca 300
 cacgcacacg ccgcttacac ccggaccgcc ggctgctgcc ccggctttac ccttcgcct 360
 cttgcggctc ttcacgcact ccattgcccg cgcgagtagc cccctgccgg cgccgccacc 420
 cccgcacggc tcgcccctgc cgcgggcgca catagggcag cagccgcacg cgtcgcggt 480
 ctgcccagc aggcagccca gcgggggcag gggcgggcag gaggccggt cgagggggcc 540
 gcaggtgtcc gaagaggagg aagaggagag gggcaggagc aggagcagca gcccagcggc 600
 gccgangagc anggcgcgca acgacggccg cttcatggcg gggcgcggtg gcagcggctn 660
 acnccggccg naatta 676

<210> 106
 <211> 225
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (2)..(24)
 <223> XAA = ANYTHING

<400> 106
 Asn Xaa Arg Pro Xaa Xaa Pro Leu Pro Pro His Pro Ala Met Lys Arg
 1 5 10 15
 Pro Ser Leu Arg Ala Xaa Leu Xaa Gly Ala Ala Gly Leu Leu Leu Leu
 20 25 30
 Leu Leu Pro Leu Ser Ser Ser Ser Ser Ser Asp Thr Cys Gly Pro Cys
 35 40 45
 Glu Pro Ala Ser Cys Pro Pro Leu Pro Pro Leu Gly Cys Leu Leu Gly
 50 55 60
 Glu Thr Arg Asp Ala Cys Gly Cys Cys Pro Met Cys Ala Arg Gly Glu
 65 70 75 80
 Gly Glu Pro Cys Gly Gly Gly Gly Ala Gly Arg Gly Tyr Cys Ala Pro

85

90

95

Gly Met Glu Cys Val Lys Ser Arg Lys Arg Arg Lys Gly Lys Ala Gly
100 105 110

Ala Ala Ala Gly Gly Pro Gly Val Ser Gly Val Cys Val Cys Lys Ser
115 120 125

Arg Tyr Pro Val Cys Gly Ser Asp Gly Thr Thr Tyr Pro Ser Gly Cys
130 135 140

Gln Leu Arg Ala Ala Ser Gln Arg Ala Glu Ser Arg Gly Glu Lys Ala
145 150 155 160

Ile Thr Gln Val Ser Lys Gly Thr Cys Glu Gln Gly Pro Ser Ile Val
165 170 175

Thr Pro Pro Lys Asp Ile Trp Asn Val Thr Gly Ala Gln Val Tyr Leu
180 185 190

Ser Cys Glu Val Ile Gly Ile Pro Thr Pro Val Leu Ile Trp Asn Lys
195 200 205

Val Lys Arg Gly His Tyr Gly Val Gln Arg Thr Glu Leu Met Pro Gly
210 215 220

Ser
225

<210> 107

<211> 267

<212> DNA

<213> Homo sapiens

<400> 107

ggatcctgta gccgtgatgg tggctcgagg agcaatccag tgcacagtaa aagagttggc 60
agtaatata gaaaagtcaa tgccagttgg ggaatcaaga cctgttttct gtcttctct 120
aagaggtgtg ctctcatgtt gttcgtagac actggagaca ctactacat attctgtacc 180
aggcaggaga tttgttaaga ccaactgcatt gtctgaagga gaaattgaca actctgcaac 240
atcttccgtc gacgcggccg cgaattc 267

<210> 108

<211> 89

<212> PRT

<213> Homo sapiens

<400> 108

Glu Phe Ala Ala Ala Ser Thr Glu Asp Val Ala Glu Leu Ser Ile Ser
1 5 10 15

Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu Pro Gly Thr Glu
20 25 30

Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln His Glu Ser Thr Pro
 35 40 45
 Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp Ser Pro Thr Gly Ile Asp
 50 55 60
 Phe Ser Asp Ile Thr Ala Asn Ser Phe Thr Val His Trp Ile Ala Pro
 65 70 75 80
 Arg Ala Thr Ile Thr Ala Thr Gly Ser
 85

<210> 109
 <211> 911
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (659)..(911)
 <223> N = A, C, G OR T/U

<400> 109
 ggatccgcca gtgaggttgc gccagtaggc aggggaagtcc tggaactgga aggtgtagac 60
 ggcgatgagg accagcatgg tgtaggccac cagcagccac cagaaggcct tgagcagctt 120
 ccgccacagg ctgtagtaga cctggaagag ggtgaggcag agcaggaaga ggaacatgta 180
 gacaatcttg tagaccacga ggcggccggc gaagctgacc acgatgaaca tgccagcaca 240
 cacatagatc cagtacttgg cgtacacgcc cttcaccagc tccccaggc tctgcaacag 300
 cgtctgcgtc cgcgtgggct ctgtgtctgc cacggtgacc tccgtcagcg cagctggaga 360
 ctctgcccac ttcagcagct tctctttcac aaactggcgc agcaggagcc agaaggtcag 420
 ggtgtagagc aacatggcac caaggtccag acaggggtag cgggtgtgct ccagccccag 480
 ctggcgcagg ctgacggggc ccagggtggt gggcagctca gggcgcaggc ccatggccca 540
 cacgtagcgt aggcagcaca gcgtcatccc atacagcagg atgcagggcg agcacagcat 600
 ggccagttgg tggcggctgc gcaccgtcca gatgaggcag gccagagcag cagtacgaan 660
 gtcagccagc tgtggtaggt gatgctncat accatcatgg caatgagcgc gcacacatag 720
 ctttgggtcc atgatgangg gggcccaggc tggggaacgg aaacnctnc ctgggctanc 780
 ccncttgggc ccacaggccn ccccaggagg gaactttgnc cgtcaattct gcncaaagca 840
 ttntnacett cggggtcggg ngctggggna ccaactgntgt aaantcccct tctggggccc 900
 tgtncacntt n 911

<210> 110
 <211> 302
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(83)
 <223> XAA = ANYTHING

<400> 110
 Xaa Xaa Thr Gly Pro Gln Lys Gly Xaa Leu Xaa Gln Trp Xaa Pro Ser
 1 5 10 15

Xaa Arg Pro Arg Arg Xaa Xaa Cys Phe Xaa Gln Asn Arg Xaa Lys Phe
20 25 30
Pro Pro Gly Xaa Ala Cys Gly Pro Lys Xaa Xaa Ser Pro Gly Arg Xaa
35 40 45
Phe Arg Ser Pro Ala Trp Ala Pro Xaa Ile Met Asp Pro Lys Leu Cys
50 55 60
Val Arg Ala His Cys His Asp Gly Met Xaa His His Leu Pro Gln Leu
65 70 75 80
Ala Asp Xaa Arg Thr Ala Ala Leu Ala Cys Leu Ile Trp Thr Val Arg
85 90 95
Ser Arg His Gln Leu Ala Met Leu Cys Ser Pro Cys Ile Leu Leu Tyr
100 105 110
Gly Met Thr Leu Cys Cys Leu Arg Tyr Val Trp Ala Met Asp Leu Arg
115 120 125
Pro Glu Leu Pro Thr Thr Leu Gly Pro Val Ser Leu Arg Gln Leu Gly
130 135 140
Leu Glu His Thr Arg Tyr Pro Cys Leu Asp Leu Gly Ala Met Leu Leu
145 150 155 160
Tyr Thr Leu Thr Phe Trp Leu Leu Leu Arg Gln Phe Val Lys Glu Lys
165 170 175
Leu Leu Lys Trp Ala Glu Ser Pro Ala Ala Leu Thr Glu Val Thr Val
180 185 190
Ala Asp Thr Glu Pro Thr Arg Thr Gln Thr Leu Leu Gln Ser Leu Gly
195 200 205
Glu Leu Val Lys Gly Val Tyr Ala Lys Tyr Trp Ile Tyr Val Cys Ala
210 215 220
Gly Met Phe Ile Val Val Ser Phe Ala Gly Arg Leu Val Val Tyr Lys
225 230 235 240
Ile Val Tyr Met Phe Leu Phe Leu Leu Cys Leu Thr Leu Phe Gln Val
245 250 255
Tyr Tyr Ser Leu Trp Arg Lys Leu Leu Lys Ala Phe Trp Trp Leu Val
260 265 270
Val Ala Tyr Thr Met Leu Val Leu Ile Ala Val Tyr Thr Phe Gln Phe
275 280 285
Gln Asp Phe Pro Ala Tyr Trp Arg Asn Leu Thr Gly Gly Ser
290 295 300

<210> 111
 <211> 818
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (701)..(817)
 <223> N = A, C, G OR T/U

<400> 111
 ggatccaggc acaatgttgt cacaatagca aaaagcaaat ttaggataa tacaatatag 60
 aaatttccca gccaatataa ccttccaaag tcgccaagta gatcaaact agtgattccc 120
 agtgttctcg acatcacagg cagagcagag ctcaaaacca agatggacac acaatttcca 180
 atgatctttg tcatagttgt gtcacttttc ttgggagtaa agtttccaaa aaatcgaagg 240
 ctatagaagc cgacaacaga ggacaccata agatagaaaa tcaaatgat ttcaagcgca 300
 gctcccacaa aaccaaactg agaaagagag gcatttccta ttccaggccc ccttggtcct 360
 tttggcattg ctgtttcatc aaccaatagg caaagaatat tacaagccac caagaggacc 420
 gagatggatg tctcaataag aaggagaacc ataacagcgg gatacaccaa atttctttcc 480
 catgctgaag ccttttttct cctctctaat tttgtcttaa gactctttac attttcaagt 540
 tcttggtcca actccattat gttgtattcc accgatgaag acagcccatt tagtcgtctc 600
 tggagtgttt cttcctctaa ggtaatgata taaatttggt catccagggtc ttcagaattg 660
 ttggcttcac tagcaactga cccatcactg tgaactacga naaanggcaa ctggtgtacn 720
 caaganaagt aacaacntcc atcatgattt caggatntaa tagggagatg nactnccana 780
 atcatttaag atnctgcttg cggatcgttg gcatgang 818

<210> 112
 <211> 254
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (8)..(38)
 <223> XAA = ANYTHING

<400> 112
 Ser Cys Gln Arg Ser Ala Ser Xaa Ile Leu Asn Asp Xaa Gly Ser Xaa
 1 5 10 15
 Ser Pro Tyr Xaa Ile Leu Lys Ser Trp Xaa Leu Leu Leu Xaa Leu Xaa
 20 25 30
 Thr Pro Val Ala Xaa Xaa Arg Ser Ser Gln Trp Val Ser Cys Ser Gln
 35 40 45
 Gln Phe Arg Pro Gly Thr Asn Leu Tyr His Tyr Leu Arg Gly Arg Ser
 50 55 60
 Thr Pro Glu Thr Thr Lys Trp Ala Val Phe Ile Gly Gly Ile Gln His
 65 70 75 80
 Asn Gly Val Gly Thr Arg Thr Lys Cys Lys Asp Ser Asp Lys Ile Arg

85

90

95

Glu Ala Lys Lys Gly Phe Ser Met Gly Lys Lys Phe Gly Val Ser Arg
 100 105 110

Cys Tyr Gly Ser Pro Ser Tyr Asp Ile His Leu Gly Pro Leu Gly Gly
 115 120 125

Leu Tyr Ser Leu Pro Ile Gly Asn Ser Asn Ala Lys Arg Asn Lys Gly
 130 135 140

Ala Trp Asn Arg Lys Cys Leu Ser Phe Tyr Val Trp Phe Cys Gly Ser
 145 150 155 160

Cys Ala Asn His Phe Asp Phe Leu Ser Tyr Gly Val Leu Cys Cys Arg
 165 170 175

Leu Leu Pro Ser Ile Phe Trp Lys Leu Tyr Ser Gln Glu Arg His Asn
 180 185 190

Tyr Asp Lys Asp His Trp Lys Leu Cys Val His Leu Gly Phe Glu Leu
 195 200 205

Cys Ser Ala Cys Asp Val Glu Asn Thr Gly Asn His Ile Ser Thr Trp
 210 215 220

Arg Leu Trp Lys Val Leu Ala Gly Lys Phe Leu Tyr Cys Ile Ile Leu
 225 230 235 240

Gln Phe Ala Phe Cys Tyr Cys Asp Asn Ile Val Pro Gly Ser
 245 250

<210> 113

<211> 905

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (708)..(900)

<223> N = A, C, G OR T/U

<400> 113

ggatccattg gggttttgggg ggaagaggaa gactgacggt cccccagga gttcaggtgc 60
 tgggcacggt gggcatgtgt gagttttgtc acaagatttg ggctcaactc tcttgtccac 120
 cttggtgttg ctgggcttgt gattcacgtt gcagatgtag gtctgggtgc ccaagctgct 180
 ggagggcacg gtcaccacgc tgctgaggga gtagagtcct gaggactgta ggacagccgg 240
 gaaggtgtgc acgccgctgg tcagggcgcc tgagttccac gacaccgtca ccggttcggg 300
 gaagtagtcc ttgaccaggc agcccagggc cgctgtgccc ccagaggtgc tcttggagga 360
 gggtgccagg ggggaagacc atggggccctt ggtggaggct gaggagacgg tgaccagggg 420
 accctggccc cactggtaac ttgtagccat ctccgcaagt ctcgcacagt aatacatggc 480
 ggtgtccgag gccttcaggc tgctccactg caggtaggcg gtactgatgg acttgctgac 540
 tgacatgggt acctggcctt ggaaggacgg gctgtatgtg gcatcagagt caccaggata 600
 gatgatcccc atccactcca gacccttccc gggcatctgg cgcaccagg cgatccagta 660

actggagaag tagtatccag agcccttaca ggagatcttc agagactncc cgggcttttt 720
cacctntggt ccagactgca cagctgcacc tcggacanac tccttggana acaaccagaa 780
ganggccagg atggcngctg acccctgatg ggganggaan aaatgaaccc tggtaancg 840
gcngnaattn ancttactnt tcttttnatt aaaaaactct tnaaaagcna tnaaagcatn 900
ccttc 905

<210> 114
<211> 301
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (2)..(66)
<223> XAA = ANYTHING

<400> 114
Arg Xaa Ala Xaa Xaa Ala Phe Xaa Glu Phe Phe Asn Xaa Lys Xaa Ser
1 5 10 15
Lys Xaa Asn Xaa Xaa Arg Leu Thr Arg Val His Xaa Phe Xaa Pro His
20 25 30
Gln Gly Ser Ala Ala Ile Leu Ala Xaa Phe Trp Leu Xaa Ser Lys Glu
35 40 45
Xaa Val Arg Gly Ala Ala Val Gln Ser Gly Pro Xaa Val Lys Lys Pro
50 55 60
Gly Xaa Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Tyr Phe Ser
65 70 75 80
Ser Tyr Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
85 90 95
Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ala Thr Tyr Ser Pro
100 105 110
Ser Phe Gln Gly Gln Val Thr Met Ser Val Asp Lys Ser Ile Ser Thr
115 120 125
Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
130 135 140
Tyr Cys Ala Arg Leu Ala Glu Met Ala Thr Ser Tyr Gln Trp Gly Gln
145 150 155 160
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
165 170 175
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
180 185 190
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser

195 200 205

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
210 215 220

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
225 230 235 240

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 245 250 255

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 260 265 270

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 275 280 285

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Asn Gly Ser
 290 295 300

<210> 115
<211> 458
<212> DNA
<213> Homo sapiens

<400> 115
ggatccggct ctgaccttct ccacgtcggc ccggggccgtc tggtaattgt ccacgctgcc 60
tgggatgtag gagcactgct ggttctggtc ccgagtgtcc tccgtgtggt acagcacagc 120
ccacctgccg gcagctgaca cgttgaccca caggcatggg tactggggca ccttcttgcc 180
cttcagctcc tcttgggtccc tgatgttggt ctcaatcagg tggcacttgg attcctgggt 240
ccacacgctt ttctggtaga ggggcagcac agtcgtgacc aggatgtagt aggtgatgac 300
ggcacacacc accatgggta caccagggca aagggtcgt gtctctcccc gcttctgggc 360
catcaccagc ttcttcacca tattcactgg gggcagtgat catttagtct tcccggcgctc 420
ctgtgggtct tgagcagcgt cgacgcggcc gcgaattc 458

<210> 116
<211> 151
<212> PRT
<213> Homo sapiens

<400> 116
Ile Arg Gly Arg Val Asp Ala Ala Gln Asp Pro Gln Asp Ala Gly Lys
1 5 10 15

Thr Lys Ser Leu Pro Pro Val Asn Met Val Lys Lys Leu Val Met Ala
 20 25 30

Gln Lys Arg Gly Glu Thr Arg Ala Leu Cys Leu Gly Val Thr Met Val
 35 40 45

Val Cys Ala Val Ile Thr Tyr Tyr Ile Leu Val Thr Thr Val Leu Pro
 50 55 60

Leu Tyr Gln Lys Ser Val Trp Thr Gln Glu Ser Lys Cys His Leu Ile
 65 70 75 80
 Glu Thr Asn Ile Arg Asp Gln Glu Glu Leu Lys Gly Lys Lys Val Pro
 85 90 95
 Gln Tyr Pro Cys Leu Trp Val Asn Val Ser Ala Ala Gly Arg Trp Ala
 100 105 110
 Val Leu Tyr His Thr Glu Asp Thr Arg Asp Gln Asn Gln Gln Cys Ser
 115 120 125
 Tyr Ile Pro Gly Ser Val Asp Asn Tyr Gln Thr Ala Arg Ala Asp Val
 130 135 140
 Glu Lys Val Arg Ala Gly Ser
 145 150

<210> 117
 <211> 715
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (669)..(710)
 <223> N = A, C, G OR T/U

<400> 117
 ggatcctgct tccaggcgct tctcattctc atggatcttc ttcacccgca gcttctgctt 60
 ctcagtcaga aggttggtgt cctcatccct ctcatacagg gtgaccagga cgttcttgag 120
 ccagtcctgc atgcgcaggg ggaattcggg cagctcagag tccaggcaag gggggatgta 180
 tttgcaaggc ccgatgtagt ccagggtggag cttgtggccc ttcttggtgc cctccagggt 240
 gcactttgtg gcaaagaagt ggcaggaaga gtcgaagggtc ttgttgatcat tgctgcacac 300
 cttctcaaac tcgccaatgg gggctgggca gctgggtggg tcttggcaca cgcacatggg 360
 ggtgtgtgtc tcatccagct cgcacacctt gccgtgtttg cagtgggtgt tctggcaggg 420
 attttcggcc accacctcct cttcggtttc ctctgcacca tcatcaaatt ctctacttc 480
 cacctggaca ggattagctc ccacagatac ctcagtcacc tctgccacag tttcttccac 540
 cacctctgtc tcatcaggca gggcttcttg ctgagggggt gccaaaggccc tcccggccag 600
 gcaaaggaga aagaagatcc aggccctcat ggtgctggga accctcagtg gcaggcaggc 660
 aggcggcgang canancgcgc tctccgggca gtctggtcga cncggccgcn aattc 715

<210> 118
 <211> 238
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (2)..(16)
 <223> XAA = ANYTHING

<400> 118

Asn Xaa Arg Pro Xaa Arg Pro Asp Cys Pro Glu Ser Ala Xaa Cys Xaa
 1 5 10 15
 Pro Pro Ala Cys Leu Pro Leu Arg Val Pro Ser Thr Met Arg Ala Trp
 20 25 30
 Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala Pro Gln
 35 40 45
 Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr Val Ala
 50 55 60
 Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val Glu Val
 65 70 75 80
 Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Glu Val Val Ala
 85 90 95
 Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val Cys Glu
 100 105 110
 Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro Thr Ser
 115 120 125
 Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn Asp Asn
 130 135 140
 Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys Thr Leu
 145 150 155 160
 Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile Gly Pro
 165 170 175
 Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu Phe Pro
 180 185 190
 Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu Tyr Glu
 195 200 205
 Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu Arg Val
 210 215 220
 Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Ser
 225 230 235

<210> 119

<211> 467

<212> DNA

<213> Homo sapiens

<400> 119

ggatcccttg tgggtccgcc ctccgaggta tccgtccagt ggccgcgggc ccgcggggac 60
 cccggggcgc tgctgggtgc tgctctccgc cgccgggtgc gagctgccgg tggccgacgc 120
 ctgctgctgc tggtgctgct gctgctgctg ctgctgcggg ggccgctcct tctggccgcc 180

gaggctgctg tacactagca acaagctggt gcacatggtg gtgagcgcta aacacactgc 240
cagaccatgg cgcacaggg tcttcatttt gggcacctct tttgtgcaga atcctcaggc 300
tcgcgcgtcc ggggccactt tttcctggag ggtttccatg atgggtaatg gggcggaggc 360
ggctctgatt tttgccagc agccggccgc ggcagatcgc gcgcgggagc cgcgggaccc 420
gggaagcgcg gctgttcag agattaggtc gacgcggccg cgaattc 467

<210> 120
<211> 154
<212> PRT
<213> Homo sapiens

<400> 120
Ile Arg Gly Arg Val Asp Leu Ile Ser Ala Thr Ala Ala Leu Pro Gly
1 5 10 15
Ser Arg Gly Ser Arg Ala Arg Ser Ala Ala Ala Gly Cys Trp Ala Lys
20 25 30
Ile Arg Ala Ala Ser Ala Pro Leu Pro Ile Met Glu Thr Leu Gln Glu
35 40 45
Lys Val Ala Pro Asp Ala Arg Ala Gly Phe Cys Thr Lys Glu Val Pro
50 55 60
Lys Met Lys Thr Leu Met Arg His Gly Leu Ala Val Cys Leu Ala Leu
65 70 75 80
Thr Thr Met Cys Thr Ser Leu Leu Leu Val Tyr Ser Ser Leu Gly Gly
85 90 95
Gln Lys Glu Arg Pro Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln
100 105 110
Gln Gln Ala Ser Ala Thr Gly Ser Ser Gln Pro Ala Ala Glu Ser Ser
115 120 125
Thr Gln Gln Arg Pro Gly Val Pro Ala Gly Pro Arg Pro Leu Asp Gly
130 135 140
Tyr Leu Gly Val Ala Asp His Lys Gly Ser
145 150

<210> 121
<211> 859
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (677)..(857)
<223> N = A, C, G, OR T/U

<400> 121

```

ggatccacac acatcctcac cccacagnaa actgctggac aactgaaga aactgaataa 60
aacagatgaa gaaataagca gttaaaaaaa taagtcgccc ctccaaaaca cgcccccatc 120
ccacagcgct cgcagcttc ccaccaccgc cgcctcagt tcctttgcgt ctgttgccctc 180
cccagccctg cagccctgg ctggcactgt tgcgcgtgca ttctcgtgtt cagtgatgcc 240
ctcttcttgt ttgaaacaaa agaaaataat gcattgtgtt ttttaaaaag agtatcttat 300
acatgtatcc taaaaagaga agctcatgtg caattgggtg acagcaggag aaatttcttg 360
actgttagga tgaatggacg ccttctcccc gttatttaag atttgtgacc ttgtacataa 420
ccctgggtga cgtgcacatt gcttgggtat ggaacggtag aaatttgggt gtttttaaaa 480
ccttggttgg ggttgcttct gtccttggtg agaatacatag agatgtctgt gttcttgagg 540
tatttcacac tgaggactaa tctgctatct tcattccagt ccctaccctt cagtgcctgc 600
tctcatccaa ataacctggg aggtgacaat caggatatct caggagggtcc aagggtggaac 660
agacctcttt gccttttcca gcgtctcata cccccggtag tgcantctgtg ggtggagggt 720
gggggtgtctg caccaantca gggcagcgtc ctntctccna gcctgtactg gccccctccc 780
ancctgggtc cccagggctg ggatccccag ggantncttc cntttaanna aagggccctg 840
acnnggaaaa acaactncc 859

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<210> 122

<211> 278

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (1) .. (61)

<223> XAA = ANYTHING

<400> 122

```

Xaa Val Val Phe Pro Xaa Gln Gly Pro Xaa Xaa Lys Xaa Lys Xaa Ser
  1              5              10              15

```

```

Leu Gly Ile Pro Ala Leu Gly Thr Gln Xaa Gly Lys Gly Pro Val Gln
      20              25              30

```

```

Ala Xaa Lys Xaa Asp Ala Ala Leu Xaa Trp Cys Arg His Pro Ser Leu
      35              40              45

```

```

His Pro Gln Xaa His Tyr Arg Gly Tyr Glu Thr Leu Xaa Lys Ala Lys
      50              55              60

```

```

Arg Ser Val Pro Pro Trp Thr Ser Asp Ile Leu Ile Val Thr Ser Gln
      65              70              75              80

```

```

Val Ile Trp Met Arg Ala Gly Thr Glu Gly Gly Leu Glu Arg Gln Ile
      85              90              95

```

```

Ser Pro Gln Cys Glu Ile Leu Gln Glu His Arg His Leu Tyr Asp Ser
      100              105              110

```

```

Gln Gln Gly Gln Glu Gln Pro Gln Thr Arg Phe Lys His Pro Asn Phe
      115              120              125

```

```

Tyr Arg Ser Ile Pro Lys Gln Cys Ala Arg His Pro Gly Leu Cys Thr
      130              135              140

```

Arg Ser Gln Ile Leu Asn Asn Gly Glu Lys Ala Ser Ile His Pro Asn
 145 150 155 160

Ser Pro Glu Ile Ser Pro Ala Val His Gln Leu His Met Ser Phe Ser
 165 170 175

Phe Asp Thr Cys Ile Arg Tyr Ser Phe Lys Thr Gln Cys Ile Ile Phe
 180 185 190

Phe Cys Phe Lys Gln Glu Glu Gly Ile Thr Glu His Glu Asn Ala Ala
 195 200 205

Ala Thr Val Pro Ala Arg Ala Cys Arg Ala Gly Glu Ala Thr Asp Ala
 210 215 220

Lys Glu Leu Arg Arg Ala Val Val Gly Ser Cys Gly Ala Leu Trp Asp
 225 230 235 240

Gly Gly Val Phe Trp Arg Gly Asp Leu Phe Phe Leu Leu Ile Ser Ser
 245 250 255

Ser Val Leu Phe Ser Phe Phe Ser Val Ser Ser Ser Xaa Leu Trp Gly
 260 265 270

Glu Asp Val Cys Gly Ser
 275

<210> 123
 <211> 478
 <212> DNA
 <213> Homo sapiens

<400> 123
 ggatccatca tatgtgtcta ctgtggggac aactggagtg aaaacttcgg ttgctggcag 60
 gtccgtggga aaatcagtga ccagttcatc agattcatca gaatggtgag actcatcaga 120
 ctggtgagaa tcatcagtg catctacatc atcagagtcg tttgagtcaa tggagtcctg 180
 gctgtccaca tggatcatcat catcttcatc atccatatca tccatgtggt catggctttc 240
 gttggactta cttggaagg tctgtggggc taggagattc tgcttctgag atgggtcagg 300
 gtttagccat gtggccacag catctgggta tttgttgtaa agctgctttt cctcagaact 360
 tccagaatca gcctgtttta ctggtatggc acaggtgatg cctaggaggc aaaagcaaat 420
 cactggtcga cgcgccgcg aattcgcgcc cgcgtcgacg tcgacgcgcc gcgaattc 478

<210> 124
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 124
 Asn Ser Arg Arg Val Asp Val Asp Ala Ala Ala Asn Ser Arg Pro Arg
 1 5 10 15

Arg Pro Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala Ile Pro
 20 25 30

Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu Tyr Asn
35 40 45

Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro Ser Gln
50 55 60

Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser Asn Glu
65 70 75 80

Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His
85 90 95

Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp
100 105 110

Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu
115 120 125

Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu
130 135 140

Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Ser
145 150 155

<210> 125

<211> 889

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (743)..(888)

<223> N = A, C, G OR T/U

<400> 125

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ggatccgctt ttgtgtgcaa acaatggcaa acaatggcag caaaccacag cccagctgac 60
agccattaag atggagtatt catttgtcat ggtgggtaaa ggctcttcaa tagctgctaa 120
tcaaaataga gaaaaatgaa tgtatggcac gatgcaactc taataagact ggggtgtccaa 180
atgagtgact ccacataggt atgcgtaagg cgtacatgga atgaccttct ctttgaactt 240
gctgccaccg tggagcagca tatctccctt gagaacttcc tcccttgact tccgaggaga 300
tcttactctc tcatttctga ccgaccttcc tttaccttgt tcttcccacc cattccctca 360
atgagacagt cccccagcca ctgctctctg ttcaaattcc ctgctgact gatgccctgg 420
ggaagatccc ttctcctaaa tcttatgggg atttaagaat attacttgtc cagctgcagc 480
caaagtggac atggcattgg gacgcagatg tgcttgtgct tacctaaata ctcattctaa 540
agatggcaaa gactgggact ttcatgtatt cattccgac actctcattc ccagatactg 600
agctagaagc tgggtgatgca gatacaagac tgggtgtccc aaggaactta aaaaaccatc 660
ctccctgtca ctgtagtggc tgccatgggt tgactataacc aagtactctg ctaactgctt 720
tacttatgca atcccaccta atnctcacag caaccagtg agngggctac taggataatt 780
ccttttcctt ttcctttttt tttttttttg anacggattt nctnttggtg cccagctgga 840
ggcaangggc gaactcgggt actgaaaccc ctntctctng gtnancnt 889
```

<210> 126

<211> 285
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(47)
 <223> XAA = ANYTHING

<400> 126

Xaa	Xaa	Thr	Xaa	Glu	Xaa	Gly	Phe	Gln	Pro	Ser	Ser	Pro	Xaa	Ala	Ser	1	5	10	15
Ser	Trp	Ala	Thr	Xaa	Xaa	Asn	Pro	Xaa	Gln	Lys	Lys	Lys	Lys	Arg	Lys	20	25	30	
Arg	Lys	Arg	Asn	Tyr	Pro	Ser	Ser	Xaa	Leu	Thr	Gly	Leu	Leu	Xaa	Leu	35	40	45	
Gly	Gly	Ile	Ala	Val	Lys	Gln	Leu	Ala	Glu	Tyr	Leu	Val	Ser	Thr	His	50	55	60	
Gly	Ser	His	Tyr	Ser	Asp	Arg	Glu	Asp	Gly	Phe	Leu	Ser	Ser	Leu	Gly	65	70	75	80
Thr	Pro	Val	Leu	Tyr	Leu	His	His	Gln	Leu	Leu	Ala	Gln	Tyr	Leu	Gly	85	90	95	
Met	Arg	Val	Ser	Glu	Met	Asn	Thr	Lys	Ser	Gln	Ser	Leu	Pro	Ser	Leu	100	105	110	
Glu	Val	Phe	Arg	Ala	Gln	Ala	His	Leu	Arg	Pro	Asn	Ala	Met	Ser	Thr	115	120	125	
Leu	Ala	Ala	Ala	Gly	Gln	Val	Ile	Phe	Leu	Asn	Pro	His	Lys	Ile	Glu	130	135	140	
Lys	Gly	Ser	Ser	Pro	Gly	His	Gln	Ser	Arg	Arg	Glu	Phe	Glu	Gln	Arg	145	150	155	160
Ala	Val	Ala	Gly	Gly	Leu	Ser	His	Gly	Asn	Gly	Trp	Glu	Glu	Gln	Gly	165	170	175	
Lys	Glu	Arg	Ser	Val	Arg	Asn	Glu	Arg	Val	Arg	Ser	Pro	Arg	Lys	Ser	180	185	190	
Arg	Glu	Glu	Val	Leu	Lys	Gly	Asp	Met	Leu	Leu	His	Gly	Gly	Ser	Lys	195	200	205	
Phe	Lys	Glu	Lys	Val	Ile	Pro	Cys	Thr	Pro	Tyr	Ala	Tyr	Leu	Cys	Gly	210	215	220	
Val	Thr	His	Leu	Asp	Thr	Gln	Ser	Tyr	Ser	Cys	Ile	Val	Pro	Tyr	Ile	225	230	235	240

His Phe Ser Leu Phe Leu Ala Ala Ile Glu Glu Pro Leu Pro Thr Met
 245 250 255

Thr Asn Glu Tyr Ser Ile Leu Met Ala Val Ser Trp Ala Val Val Cys
 260 265 270

Cys His Cys Leu Pro Leu Phe Ala His Lys Ser Gly Ser
 275 280 285

<210> 127
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 127
 ggatccctca acgccggtgg tttcttggtc ggtgggtgac tctgagccgt cggggcagac 60
 gggacagcac tcgccctcgg ggacttcggc gccggggcag ttcttggtct cgtcacagat 120
 cacgtcatcg cacaacacct tgccgttgtc gcagacgcag atccggcagg gtcggggttt 180
 ccacacgtct cggtcatggt acctgaggcc gttctgtacg caggtgattg gtgggatgac 240
 ttcgtcttgg ccctcgactt ggccttcttc ttggccgtgc gtcaggaggg cgggtggccgc 300
 taagaggagc aggagccgga gtcgacgcgg ccgcgaatt 339

<210> 128
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 128
 Asn Ser Arg Pro Arg Arg Leu Arg Leu Leu Leu Leu Ala Ala Thr
 1 5 10 15
 Ala Leu Leu Thr His Gly Gln Glu Glu Gly Gln Val Glu Gly Gln Asp
 20 25 30
 Glu Asp Ile Pro Pro Ile Thr Cys Val Gln Asn Gly Leu Arg Tyr His
 35 40 45
 Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Arg Ile Cys Val Cys Asp
 50 55 60
 Asn Gly Lys Val Leu Cys Asp Asp Val Ile Cys Asp Glu Thr Lys Asn
 65 70 75 80
 Cys Pro Gly Ala Glu Val Pro Glu Gly Glu Cys Cys Pro Val Cys Pro
 85 90 95
 Asp Gly Ser Glu Ser Pro Thr Asp Gln Glu Thr Thr Gly Val Glu Gly
 100 105 110
 Ser

<210> 129
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 129
 ggatccatag caggggggctg ggcgctgggtt gggcccaaaag agatgcaagt cgccgtattc 60
 ccatagaaac agctgagtca tcagggctcc gaagcccaca accgccagaa tgaggaccag 120
 caggaccag cgggctttct tttccgcagc cttccacgcc tcaatctcat tcatgggcag 180
 ctcattggcg ggctcctctg caggcacctt cagctcctgg tacatcagtt taggcttcat 240
 cttccctcaa ggctggggga tacgcagagc ccaggtgaga aggtgggtgt gtcaggggtct 300
 ccaaaccctg aggggctctg gctcgtctct caggcgtctg ctgctacctc cgctgggccc 360
 cagctttctgt ctggacaggc tgaacgaggg tgggaggagg gggcggggcc tgtgggagct 420
 ccgcccactg cagcggggag tctgcgcagt gcgtgcccc gtccgggctc accgcagcga 480
 gaagcggggc tcggctcccc agacacggtc gctccaggtc gacgcggccg cgaattc 537

<210> 130
 <211> 176
 <212> PRT
 <213> Homo sapiens

<400> 130
 Glu Phe Ala Ala Ala Ser Thr Trp Ser Asp Arg Val Trp Gly Ala Glu
 1 5 10 15
 Pro Arg Phe Ser Leu Arg Ala Arg Thr Gly Ala Arg Thr Ala Gln Thr
 20 25 30
 Pro Arg Cys Ser Gly Arg Ser Ser His Arg Pro Arg Pro Leu Leu Pro
 35 40 45
 Pro Ser Phe Ser Leu Ser Arg Gln Lys Leu Gly Pro Ser Gly Gly Ser
 50 55 60
 Ser Arg Arg Leu Arg Ala Arg Pro Arg Pro Leu Arg Val Trp Arg Pro
 65 70 75 80
 His Thr His Leu Leu Thr Trp Ala Leu Arg Ile Pro Gln Pro Gly Lys
 85 90 95
 Met Lys Pro Lys Leu Met Tyr Gln Glu Leu Lys Val Pro Ala Glu Glu
 100 105 110
 Pro Ala Asn Glu Leu Pro Met Asn Glu Ile Glu Ala Trp Lys Ala Ala
 115 120 125
 Glu Lys Lys Ala Arg Trp Val Leu Leu Val Leu Ile Leu Ala Val Val
 130 135 140
 Gly Phe Gly Ala Leu Met Thr Gln Leu Phe Leu Trp Glu Tyr Gly Asp
 145 150 155 160
 Leu His Leu Phe Gly Pro Asn Gln Arg Pro Ala Pro Cys Tyr Gly Ser
 165 170 175

<210> 131
 <211> 392
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> (9)..(354)
 <223> N = A, C G OR T/U

<400> 131
 gaattcggnc agtggcccgnc aggaatncgg ncccggggga acctttcctg agattctgcc 60
 ccaggatgcc aactttgant nggatgaana ctacaacttg tnccttctc atctgcatct 120
 ccctgctcca gctgatggtc ccagtgaata ctgatgagac catagagatt atcgtggaga 180
 ataagggtcaa ggaacttctt gccaatccag ctaactatcc ctccactgta acgaanactc 240
 tctcttgac tagtgtcaag actatgaaca gatgggcctc ctgccctgct gggatgactg 300
 ctactgggtg tgcttggtgc ttgacctgtg gatcttgga gatccagagt gganatactt 360
 gcaactgcct gtgcttactc ctgactggat cc 392

<210> 132
 <211> 130
 <212> PRT
 <213> Mus musculus

 <220>
 <221> MOD_RES
 <222> (3)..(118)
 <223> XAA = ANYTHING

<400> 132
 Ile Arg Xaa Val Ala Arg Arg Asn Xaa Xaa Pro Gly Glu Pro Phe Leu
 1 5 10 15

 Arg Phe Cys Pro Arg Met Pro Thr Leu Xaa Xaa Met Xaa Thr Thr Thr
 20 25 30

 Cys Xaa Leu Leu Ile Cys Ile Ser Leu Leu Gln Leu Met Val Pro Val
 35 40 45

 Asn Thr Asp Glu Thr Ile Glu Ile Ile Val Glu Asn Lys Val Lys Glu
 50 55 60

 Leu Leu Ala Asn Pro Ala Asn Tyr Pro Ser Thr Val Thr Xaa Thr Leu
 65 70 75 80

 Ser Cys Thr Ser Val Lys Thr Met Asn Arg Trp Ala Ser Cys Pro Ala
 85 90 95

 Gly Met Thr Ala Thr Gly Cys Ala Cys Gly Phe Ala Cys Gly Ser Trp
 100 105 110

 Glu Ile Gln Ser Gly Xaa Thr Cys Asn Cys Leu Cys Leu Leu Leu Thr

115

120

125

Gly Ser
130

<210> 133
<211> 455
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (409)
<223> N = A, C, G OR T/U

<400> 133
gaattcgcgg ccgcgctcgac ggaaagggtca agctgggttcc aaatactaaa atacagatgt 60
catattcgggt aaaatggaaa aaatcggatg taaaatttga agatcgattc gataaatatc 120
ttgatccatc ctttttttcag cataggattc actgggttttc aattttttaat tccttcatga 180
tggtgatctt cttagtggga ttagtttcaa tgattttaat gagaacttta aggaaagatt 240
atgcccgata cagtaaagaa gaagaaatgg atgacatgga cagagaccta ggagacgagt 300
atggctggaa gcagggtgcat ggagatgtgt tcagaccgtc aagtcaccct ctgatcttct 360
cctccctcat tggctctgga tgtcagatat ttgctgtgtc tctcattgnt attattgttg 420
ccatgataga ggacttatat acagagatgg gatcc 455

<210> 134
<211> 455
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (409)
<223> N = A, C, G OR T/U

<400> 134
gaattcgcgg ccgcgctcgac ggaaagggtca agctgggttcc aaatactaaa atacagatgt 60
catattcgggt aaaatggaaa aaatcggatg taaaatttga agatcgattc gataaatatc 120
ttgatccatc ctttttttcag cataggattc actgggttttc aattttttaat tccttcatga 180
tggtgatctt cttagtggga ttagtttcaa tgattttaat gagaacttta aggaaagatt 240
atgcccgata cagtaaagaa gaagaaatgg atgacatgga cagagaccta ggagacgagt 300
atggctggaa gcagggtgcat ggagatgtgt tcagaccgtc aagtcaccct ctgatcttct 360
cctccctcat tggctctgga tgtcagatat ttgctgtgtc tctcattgnt attattgttg 420
ccatgataga ggacttatat acagagatgg gatcc 455

<210> 135
<211> 151
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES

<222> (136)
<223> XAA = ANYTHING

<400> 135
Ile Arg Gly Arg Val Asp Gly Lys Val Lys Leu Val Pro Asn Thr Lys
1 5 10 15
Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe
20 25 30
Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg
35 40 45
Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu
50 55 60
Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr
65 70 75 80
Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu
85 90 95
Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro
100 105 110
Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln
115 120 125
Ile Phe Ala Val Ser Leu Ile Xaa Ile Ile Val Ala Met Ile Glu Asp
130 135 140
Leu Tyr Thr Glu Met Gly Ser
145 150

<210> 136
<211> 490
<212> DNA
<213> Mus musculus

<400> 136
gaattcgcg cgcgctcgac ccaaattccat cactgtcttc tttaaagaga tagaagttat 60
attcagtga acgaccagtg aagtatcatg gatcatcatc ataatggttg ctgtcatgta 120
tgctggaggt cctatcagca gtatcttggt gaataaatac ggcagccgtc cagtaatgat 180
cgctgggtgt tgtctgtctg gttgcggctt gatcgagct tctttctgta acacagtaca 240
ggaactttac ttgtgcattg gtgttattgg aggtcttggg cttgctttca acttgaaccc 300
agctctgact atgattggca agtatttcta caagaagcga ccactggcca acggactggc 360
catggcaggc agccctgtgt tcctctctac cctggctcca cttaatcagg ctttctttga 420
tatttttgac tggagaggaa gcttcctaata tcttgggggc ctctctctaa attgttgtgt 480
agctggatcc 490

<210> 137
<211> 163
<212> PRT

<213> Mus musculus

<400> 137

Asn Ser Arg Pro Arg Arg Pro Lys Ser Ile Thr Val Phe Phe Lys Glu
1 5 10 15

Ile Glu Val Ile Phe Ser Ala Thr Thr Ser Glu Val Ser Trp Ile Ser
20 25 30

Ser Ile Met Leu Ala Val Met Tyr Ala Gly Gly Pro Ile Ser Ser Ile
35 40 45

Leu Val Asn Lys Tyr Gly Ser Arg Pro Val Met Ile Ala Gly Gly Cys
50 55 60

Leu Ser Gly Cys Gly Leu Ile Ala Ala Ser Phe Cys Asn Thr Val Gln
65 70 75 80

Glu Leu Tyr Leu Cys Ile Gly Val Ile Gly Gly Leu Gly Leu Ala Phe
85 90 95

Asn Leu Asn Pro Ala Leu Thr Met Ile Gly Lys Tyr Phe Tyr Lys Lys
100 105 110

Arg Pro Leu Ala Asn Gly Leu Ala Met Ala Gly Ser Pro Val Phe Leu
115 120 125

Ser Thr Leu Ala Pro Leu Asn Gln Ala Phe Phe Asp Ile Phe Asp Trp
130 135 140

Arg Gly Ser Phe Leu Ile Leu Gly Gly Leu Leu Leu Asn Cys Cys Val
145 150 155 160

Ala Gly Ser

<210> 138

<211> 358

<212> DNA

<213> Mus musculus

<400> 138

gaattcgagg ccgctttnga cgcggcgagg gcggccgagc tggatgatcgg ctggtgcatc 60
ttcgacctct tgctcctggc tattttggcc ttttgctggg tctacgttcg gaagtaccag 120
agtcagcggg aaagtggagt cgtctccact gtgacagcca ttttttccact ggctgttgct 180
ctgatcacat cagcactgct gccgggtggat atatttttgg tttcttacat gaaaaatcaa 240
aatggcacat tcaaggactg ggctgacgcc aatgtcaccg tacagattga gaataccggt 300
ctgtatggct actatactct gtattctgtc attctcttct gtgtgttctt ctggatcc 358

<210> 139

<211> 356

<212> DNA

<213> Mus musculus

<400> 139

gaattcgcgg ccgcgtcgac gttttttggt ttttgttttt gtgtttgttt ttgttttttt 60
gagccagggc aatacagaaa aaaaacaaac aaacaaacaa aatgtagtgt aaagtggcct 120
gtggttctgc tgttaaagac aggttctttc atatttctca gtctagaagt cagcagtgt 180
attgtgataa tttcatattt ggaaacctaa gtgaaacttg gtgcatgata tttattcttc 240
aaaatgcagg taagctgatg gccatatctg tctggatatg gtttgttctt tagactgagc 300
ctctgtgggt tgctaactgg gtacatgttt tattgacagc aatatgttta ggatcc 356

<210> 140

<211> 115

<212> PRT

<213> Mus musculus

<400> 140

Ile Arg Gly Arg Val Asp Val Phe Cys Phe Leu Phe Leu Cys Leu Phe
1 5 10 15
Leu Phe Phe Ala Arg Ala Ile Gln Lys Lys Asn Lys Gln Thr Asn Lys
20 25 30
Met Cys Lys Val Ala Cys Gly Ser Ala Val Lys Asp Arg Phe Phe His
35 40 45
Ile Ser Gln Ser Arg Ser Gln Gln Cys Asn Cys Asp Asn Phe Ile Phe
50 55 60
Gly Asn Leu Ser Glu Thr Trp Cys Met Ile Phe Ile Leu Gln Asn Ala
65 70 75 80
Gly Lys Leu Met Ala Ile Ser Val Trp Ile Trp Phe Val Leu Thr Glu
85 90 95
Pro Leu Trp Phe Ala Asn Trp Val His Val Leu Leu Thr Ala Ile Cys
100 105 110
Leu Gly Ser
115

<210> 141

<211> 300

<212> DNA

<213> Mus musculus

<400> 141

gaattcgcgg ccgcgtcgac ggacacttaa gagaagtata ttaaatctga tcttgctatg 60
tatcttttta aaatatagta ttaacatact aatataatgc taattgaaaa attaaagtac 120
atatttttgt gtacatgtgt gtgcatatac gcgtgtgccca tgggtgtgcgt gtggagagca 180
ggggacagct tgccatagct ggctctctac tgccatgaca tgggtcttag ggatcgagtt 240
catgccacta ggcttcatgt tacgggtctt cctggccctg taaatatttt gaagggatcc 300

<210> 142

<211> 96
 <212> PRT
 <213> Mus musculus

<400> 142
 Glu Phe Ala Ala Ala Ser Thr Asp Thr Glu Lys Tyr Ile Lys Ser Asp
 1 5 10 15
 Leu Ala Met Tyr Leu Phe Lys Ile Tyr His Thr Asn Ile Met Leu Ile
 20 25 30
 Glu Lys Leu Lys Tyr Ile Tyr Leu Cys Thr Cys Val Cys Ile Tyr Ala
 35 40 45
 Cys Ala Met Val Cys Val Trp Arg Ala Gly Asp Ser Leu Pro Leu Ala
 50 55 60
 Leu Tyr Cys His Asp Met Gly Leu Arg Asp Arg Val His Ala Thr Arg
 65 70 75 80
 Leu His Val Thr Gly Leu Pro Gly Pro Val Asn Ile Leu Lys Gly Ser
 85 90 95

<210> 143
 <211> 897
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (580)..(896)
 <223> N = A, C, G OR T/U

<400> 143
 gaattcgcgg ccgcgtcgac ggactttggt tctctagggt gacatttcct tcccattgcc 60
 atgtaggggt cagtgatgtg cagtcgcttg tggacttaac taagtttaaa ttaaaaaaat 120
 gatttttttt gtttttttaa attaaaagac attattttgt gtgagggggg aagaagagtg 180
 tgagggttaga gccccataga tactaaacta gaagtcttgt ttataatagg ttgacactgg 240
 caagttgtta atctctcagt ggtagtcttt ctatctctaa agtggtataa gtattgatgc 300
 ttgtgttgag agtatttgct aggattagaa atcattggaa ataatgaatc aagataaaaa 360
 atggcactgg aggtaggaag ctgagggcat agaatgtcac ggttctggga agttagttag 420
 aagctgagaa gttggtgata ttctggattt gctatactcg attttatctg cccatctctt 480
 gattgacact ggcatacttg gcatatagac ttccaagaaa agatgtagc tattatggaa 540
 ggagcattgt gtagagacc cggagaaagg ggtagctctn caagtaggtt ctcaattaac 600
 ataggtagag cggcgggtga cggccactgt gaactcttc ctatctactt attggtcctt 660
 tagctctcac ctacttcta ccttcttaa cccgagcacc caggagtctg ntcttcaact 720
 cttgagagaa gtaaaagatg gcttatgaaa antttantag ctgcacatag gaatgaaggt 780
 gtgggcntntg gaccngatga tgganattga atccctggcc ttactactat gggatttngg 840
 taattaaatg gcttggggaac tgaaataatt ggggggtatg aggatanttt ganannt 897

<210> 144
 <211> 357
 <212> DNA
 <213> Mus musculus

<400> 144
 gaattcgcgg ccgcgtcgac gcggcggcgg cggccgagct ggtgatcggc tggatcatct 60
 tcggcctctt gctcctggct attttggcct tttgctgggt ctacgttcgg aagtaccaga 120
 gtcagcggga aagtgaggtc gtctccactg tgacagccat tttttcactg gctgttgctc 180
 tgatcacatc agcactgctg ccggtggata tatttttggg ttcttacatg aaaaatcaaa 240
 atggcacatt caaggactgg gctgacgcca atgtcaccgt acagattgag aataccgttc 300
 tgtatggcta ctatactctg tattctgtca ttctcttctg tgtgttcttc tggatcc 357

<210> 145
 <211> 115
 <212> PRT
 <213> Mus musculus

<400> 145
 Glu Phe Ala Ala Ala Ser Thr Arg Arg Arg Arg Pro Ser Trp Ser Ala
 1 5 10 15
 Gly Ala Ser Ser Ala Ser Cys Ser Trp Leu Phe Trp Pro Phe Ala Gly
 20 25 30
 Ser Thr Phe Gly Ser Thr Arg Val Ser Gly Lys Val Arg Ser Ser Pro
 35 40 45
 Leu Gln Pro Phe Phe His Trp Leu Leu Leu Ser His Gln His Cys Cys
 50 55 60
 Arg Trp Ile Tyr Phe Trp Phe Leu Thr Lys Ile Lys Met Ala His Ser
 65 70 75 80
 Arg Thr Gly Leu Thr Pro Met Ser Pro Tyr Arg Leu Arg Ile Pro Phe
 85 90 95
 Cys Met Ala Thr Ile Leu Cys Ile Leu Ser Phe Ser Ser Val Cys Ser
 100 105 110
 Ser Gly Ser
 115

<210> 146
 <211> 346
 <212> DNA
 <213> Mus musculus

<400> 146
 gaattcgcgg ccgcgtcgac ctataatctg tctacctatc taaccacccat acatctatct 60
 catctatata ttcacttata cacctattta agtatctatt gacctatgta gctactatgt 120
 atctacccat gtgtctacct gtgtgtctat ttatcacata tctgtctgtc tgtctgtcta 180
 tcatttgctt atctacttat ttacttagga aacaaacatg gagatgtttt tgttcaagtg 240

caaggatttt ataaaagcat ctataaaaat ctgtgtcatg gtctttgtcc tcattgatat 300
aggactgttt agtaccagca cctgctatac tctagccact ggatcc 346

<210> 147
<211> 112
<212> PRT
<213> Mus musculus

<400> 147
Asn Ser Arg Pro Arg Arg Pro Ile Ile Cys Leu Pro Ile Pro Pro Tyr
1 5 10 15
Ile Tyr Leu Ile Tyr Ile Phe Ile Tyr Thr Pro Ile Val Ser Ile Asp
20 25 30
Leu Cys Ser Tyr Tyr Val Ser Thr His Val Ser Thr Cys Val Ser Ile
35 40 45
Tyr His Ile Ser Val Cys Leu Ser Val Tyr His Leu Pro Ile Tyr Leu
50 55 60
Phe Thr Glu Thr Asn Met Glu Met Phe Leu Phe Lys Cys Lys Asp Phe
65 70 75 80
Ile Lys Ala Ser Ile Lys Ile Cys Val Met Val Phe Val Leu Ile Asp
85 90 95
Ile Gly Leu Phe Ser Thr Ser Thr Cys Tyr Thr Leu Ala Thr Gly Ser
100 105 110

<210> 148
<211> 962
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (672)..(961)
<223> N = A, C, G OR T/U

<400> 148
gaattcgcg cgcgctcgac gtagactgtt tggcttggtt caaggattca gcaaattctct 60
gcaagttagt gctttgcatg gtgcctggcc catggtaaat aaatgtcctg gcaagttaaa 120
gtcttcagag ctctatatac atttgaaccc agaactccag atgaattata ctttgaagaa 180
ggagacatta tctacatcac tgacatgagt gataaccagct ggtggaaagg gacatgcaag 240
ggcagaacag gactgatccc gagcaactat gtggctgagc aggcagaatc cattgacaat 300
ccattgcatg aagctgcaaa aagaggcaac ctgagctggt tgagggagtg cttggacaac 360
cgggtgggtg tgaacggcct ggacaaagct ggaagcacag ccctgtactg ggccctgccac 420
ggtggccata aagacatagt ggaggttctg tttactcagc ccgaatgtgg agctgaacca 480
gcagaataag ctgggagaca cagctctgca cgcggctgcc tggaaggggt atgcagacat 540

tgtccagttg ctactggcaa aagggtgag gacagacttg agaaacaatg agaagaagct 600
gccttgaca tggccaccaa cgctgcctgt gcatcgcttc tgaagaagaa gcagcaggga 660
acagatgggg cntcgaacgt taagcaacgc ccgaaggact tancctcgat gaccaaagac 720
ntcagactgg attccccccg ggggccgggt ttgaatgggt ggccctaaact ttcttttngc 780
ttttngncaa tttccgggaa ccctnggggt ggnttngncc cnaaaaaagt nnttgataa 840
ccnggtggcn tttttaaag gtctgggatt gaaacccga anacttgggt ggcaactggg 900
ggattcccaa cccagaaaa acccttgggt naaaggtaaa aagnnagnct tgaaaaatcc 960
nt 962

<210> 149
<211> 296
<212> DNA
<213> Mus musculus

<400> 149
gaattcgcgg cccgcgtcga cttttttttt ttttgactg tcctaaattg tttattggat 60
atgaatttta caaatatcac gtgtattagc ggtaacgggt gagctggaga gtattgcgcc 120
ttctccaggc tgcacggcgg gaaccaccaa tagtgtgggt gaacttgtgg ccctttccaa 180
ggccacggct ctttcggcca gcagatgtca gccacgcat ctctctgtgt ttgtggactg 240
gtttgtgat ccactgggtg tcaggatttc ttctgatagc tttatggaac ggatcc 296

<210> 150
<211> 67
<212> PRT
<213> Mus musculus

<400> 150
Arg Trp Ser Trp Arg Val Leu Arg Leu Leu Gln Ala Ala Arg Arg Glu
1 5 10 15
Pro Pro Ile Val Trp Trp Asn Leu Trp Pro Phe Pro Arg Pro Arg Leu
20 25 30
Phe Arg Pro Ala Asp Val Ser Pro Arg Ile Ser Leu Cys Leu Trp Thr
35 40 45
Gly Leu Val Ile His Trp Val Ser Gly Phe Leu Leu Ile Ala Leu Trp
50 55 60
Asn Gly Ser
65

<210> 151
<211> 356
<212> DNA
<213> Mus musculus

<400> 151
gaattcgcgg cccgcgtcga gttttttgtt ttttgttttt gtgtttgttt ttgttttttt 60
gagccagggc aatacagaaa aaaaacaaac aaacaaacaa aatgtagtgt aaagtggcct 120
gtggttctgc tgtaaagac aggttctttc atatttctca gtctagaagt cagcagtgtg 180
attgtgataa tttcatattt ggaaacctaa gtgaaacttg gtgcatgata tttattcttc 240

aaaatgcagg taagctgatg gccatatctg tctggatatg gtttgttctt tagactgagc 300
ctctgtgggtt tgctaactgg gtacatgttt tattgacagc aatatgttta ggatcc 356

<210> 152

<211> 669

<212> DNA

<213> Mus musculus

<400> 152

gaattcgcgg cccgcgtcga cctctctgtg aggagtgcag aaacatagtg ttcaaaatgc 60
ctgctgaaat gcaagcccct cagtggctcc tgctgctact gggtatcctg ccagccacag 120
gctcagaccc tgtgctctgc ttcacccagt atgaggagtc ctctggcagg tgcaaaggcc 180
tacttgggag agacatcagg gtagaagact gctgtctcaa cgctgcctat gccttccagg 240
agcatgatgg tggcctctgt caggcatgca ggtctccaca atggtcagca tggtccttat 300
gggggcccctg ctcagttaca tgttctgagg ggtcccagct gcgacacagg cgctgtgtgg 360
gcagaggtgg tcagtgtctt gagaatgtgg ctccctggaac tcttgagtgg cagctacagg 420
cctgtgagga ccagccatgc tgtccagaga tgggtggctg gtctgagtgg ggaccctggg 480
ggccttgctc tgtcacatgc tccaaaggaa cccagatccg tcaacgagta tgtgataatc 540
ctgctcctaa gtgtggggggc cactgcccag gaagaggccc agcaatcaca ggcttgtga 600
caccagaag acctgccccca cacatggggc tgggcatcct ggggcccctg gagcccttgt 660
tcaggatcc 669

<210> 153

<211> 220

<212> PRT

<213> Mus musculus

<400> 153

Glu Phe Ala Ala Arg Val Asp Leu Ser Val Arg Ser Ala Glu Thr Cys
1 5 10 15
Ser Lys Cys Leu Leu Lys Cys Lys Pro Leu Ser Gly Ser Cys Cys Tyr
20 25 30
Trp Leu Ser Cys Gln Pro Gln Ala Gln Thr Leu Cys Ser Ala Ser Pro
35 40 45
Ser Met Arg Ser Pro Leu Ala Gly Ala Lys Ala Tyr Leu Gly Glu Thr
50 55 60
Ser Gly Lys Thr Ala Val Ser Thr Leu Pro Met Pro Ser Arg Ser Met
65 70 75 80
Met Val Ala Ser Val Arg His Ala Gly Leu His Asn Gly Gln His Gly
85 90 95
Pro Tyr Gly Gly Pro Ala Gln Leu His Val Leu Arg Gly Pro Ser Cys
100 105 110
Asp Thr Gly Ala Val Trp Ala Glu Val Val Ser Ala Leu Arg Met Trp
115 120 125
Leu Leu Glu Leu Leu Ser Gly Ser Tyr Arg Pro Val Arg Thr Ser His

130 135 140

Ala Val Gln Arg Trp Val Ala Gly Leu Ser Gly Asp Pro Gly Gly Leu
 145 150 155 160

Ala Leu Ser His Ala Pro Lys Glu Pro Arg Ser Val Asn Glu Tyr Val
 165 170 175

Ile Ile Leu Leu Leu Ser Val Gly Ala Thr Ala Gln Glu Glu Ala Gln
 180 185 190

Gln Ser Gln Ala Leu His Pro Glu Asp Leu Pro His Thr Trp Ala Trp
 195 200 205

Ala Ser Trp Gly Pro Trp Ser Pro Cys Ser Gly Ser
 210 215 220

<210> 154
 <211> 179
 <212> DNA
 <213> Mus musculus

<400> 154
 gaattcgggc ccgcgggcac ttctcttgt ggaatgttta aaaagtttagc ctactaaaga 60
 aaacagtcga cttcttgtga aggttttggg gaaatatgta tcagttcggt ttatttgggt 120
 attcaataat atccttggtg ataatgctga ctccatgggt tctgatccca caaggatcc 179

<210> 155
 <211> 33
 <212> PRT
 <213> Mus musculus

<400> 155
 Arg Phe Trp Arg Asn Met Tyr Gln Phe Val Leu Phe Gly Tyr Ser Ile
 1 5 10 15

Ile Ser Leu Val Ile Met Leu Thr Pro Trp Leu Leu Ile Pro Gln Gly
 20 25 30

Ser

<210> 156
 <211> 889
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (1)..(203)
 <223> N = A, C, G OR T/U

<400> 156
 nggggggcccg ttccggnccan angttggctc ccgttatatt gtnaaaactt gcggcgaatg 60
 gcttgccggtt cctcgnctt acggatngcc gttcccgtt gcagggctng cttcatngc 120
 ntccctgcgag tcttctgatt gaaaaggaag agtaagctga tttcccatgg ccaagnccac 180
 ttctgtacct ggggtggctt ccntgggttc ctgctgtcca ggcatttctg cttccagcaa 240
 ggcagcccaa aggcaggtat gtcaagtggg atgccagagt cctcgggtgga agagtgactt 300
 gtcctagcct cctcctcctc ttgctgtctca gcctagtggg ccagctagca aggaagtcca 360
 ttgctgcttc tctctgacgc agacaccacc cactgtctgg agtgaagccg cctgcctttt 420
 cttcctagag cactggttct caacaccctt tgggcgtcct atatccgata tctgcatat 480
 ccaatatatta catgacgatt cacaacaggc gcaaaattac aggtatgaag tagcaacaaa 540
 ataacttttag ggttggggat caccacgaca tgaggaacca tgtaaagag tctcagcgat 600
 aggcagggtt agagggcgcca tcttagagct atgaccagtc agcgagggcc ttgcatacct 660
 ccccgccaaa ggaagctcag ctcaggagt ggaatattca aagaatttgg ccttttgagt 720
 agtttagctt atcctgccat tagcagaaaa tattgactgg aggggtggat tcattctaca 780
 tgttttaatt ttgaaaagta tctgtattgt gagcatatgt gtgtatcttt ggatgatttg 840
 tgcgtatgat tgctgggtgcc cacagagacc agcagagggc aatggatcc 889

<210> 157
 <211> 54
 <212> PRT
 <213> Mus musculus

<400> 157
 Leu Ile Leu Pro Leu Ala Glu Asn Ile Asp Trp Arg Gly Gly Phe Ile
 1 5 10 15
 Leu His Val Leu Ile Leu Lys Ser Ile Cys Ile Val Ser Ile Cys Val
 20 25 30
 Tyr Leu Trp Met Ile Cys Ala Tyr Asp Cys Trp Cys Pro Gln Arg Pro
 35 40 45
 Ala Glu Gly Asn Gly Ser
 50

<210> 158
 <211> 179
 <212> DNA
 <213> Mus musculus

<400> 158
 gaattcaaaa aggaagagta agcttgaatt cgggacagcg gggagtcttg aggcgcaatg 60
 gatggttttg cttttatttg tgtttgataa ccatagtcgg ttatggcgac tgctatggag 120
 atgtaggcaa ggcagcctcc tgtgtgacat tcaactgtaa ccctggagat gctggatcc 179

<210> 159
 <211> 59
 <212> PRT
 <213> Mus musculus

<400> 159
 Ile Gln Lys Gly Arg Val Ser Leu Asn Ser Gly Gln Arg Gly Val Leu

1 5 10 15
 Arg Arg Asn Gly Trp Phe Cys Phe Tyr Leu Cys Leu Ile Thr Ile Val
 20 25 30
 Gly Tyr Gly Asp Cys Tyr Gly Asp Val Gly Lys Ala Ala Ser Cys Val
 35 40 45
 Thr Phe Thr Val Asn Pro Gly Asp Ala Gly Ser
 50 55

<210> 160
 <211> 215
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (9) .. (27)
 <223> N = A, C, G OR T/U

<400> 160
 tgcttcncnc caagctttcc aggtgagaga taagggnac tcttgagtc aactttcacg 60
 ggtcttgatt taaaaaggaa tcacaggtcc catatccatt acttttccta ttgttgagaa 120
 caattttttt tcttttgaag atttatttat ttattttatg tgtatgcata cactatagct 180
 atcttcagac tcaccagaag agggcacttg gatcc 215

<210> 161
 <211> 69
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (2) .. (11)
 <223> XAA = ANYTHING

<400> 161
 Leu Xaa Xaa Lys Leu Ser Arg Glu Ile Arg Xaa Thr Leu Gly Val Asn
 1 5 10 15
 Phe His Gly Ser Phe Lys Lys Glu Ser Gln Val Pro Tyr Pro Leu Leu
 20 25 30
 Phe Leu Leu Leu Arg Thr Ile Phe Phe Leu Leu Lys Ile Tyr Leu Phe
 35 40 45
 Ile Leu Cys Val Cys Ile His Tyr Ser Tyr Leu Gln Thr His Gln Lys
 50 55 60
 Arg Ala Leu Gly Ser
 65

<210> 162
<211> 110
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (21)
<223> N = A, C, G OR T/U

<400> 162
aggagcccag gagaatctga ncaatgagga aaaagatcat aaccatattt aagacattaa 60
acaaacaaat aattgtcttt atgcaaatag taacatcgcc agctggatcc 110

<210> 163
<211> 34
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (28)
<223> XAA = ANYTHING

<400> 163
Ala Gly Asp Val Thr Ile Cys Ile Lys Thr Ile Ile Cys Leu Phe Asn
1 5 10 15
Val Leu Asn Met Val Met Ile Phe Phe Leu Ile Xaa Gln Ile Leu Leu
20 25 30
Gly Ser

<210> 164
<211> 311
<212> DNA
<213> Mus musculus

<400> 164
gaattcaggc ccgcgggggtt catgtaagtg aaggtggagt agagccctga gccctggccg 60
gctgcgtgac tgtagtagga gccggagttc tgatggtcag cgtagtcgta ttgcgagcgg 120
gtgatgggagc ggtaggagggt gctgtagtga ggaaggttga aggggctgta ggagatctgt 180
tgccgggaggt gctgctgctg ctcgctgtag tggctggggc tcagctgctc cgtcttgatg 240
tgcggtcgcgt gggactggcc tggctcgcgtg ctcagcgtgg tgagcgtgtg tgccctgctac 300
tgtcaggatc c 311

<210> 165
<211> 102
<212> PRT
<213> Mus musculus

<400> 165

Ile Gln Ala Arg Gly Val His Val Ser Glu Gly Gly Val Glu Pro Ala
1 5 10 15

Leu Ala Gly Cys Val Thr Val Val Gly Ala Gly Val Leu Met Val Ser
20 25 30

Val Val Val Leu Arg Ala Gly Asp Gly Arg Val Gly Gly Ala Val Val
35 40 45

Arg Lys Val Glu Gly Ala Val Gly Asp Leu Leu Arg Gly Val Leu Leu
50 55 60

Leu Leu Ala Val Val Ala Gly Ala Gln Leu Leu Arg Leu Asp Val Arg
65 70 75 80

Ser Leu Gly Leu Ala Trp Leu Ala Ala Gln Arg Gly Glu Arg Val Cys
85 90 95

Leu Leu Leu Ser Gly Ser
100

<210> 166

<211> 113

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (1)..(24)

<223> XAA = ANYTHING

<400> 166

Xaa Val Ser Xaa Asn Ser Gly Xaa Xaa Arg Gly Val Xaa Leu Gly Leu
1 5 10 15

Arg Ser Val Ala Xaa Gly Phe Xaa Asp Thr Glu Val Thr Thr Pro Met
20 25 30

Gly Thr Ala Glu Val Ala Pro Asp Thr Ser Pro Arg Ser Gly Pro Ser
35 40 45

Cys Trp His Arg Leu Val Gln Val Phe Gln Ser Lys Gln Phe Arg Ser
50 55 60

Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe Phe Gln Met Asn Gln
65 70 75 80

Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val Leu Leu Met Ala Val
85 90 95

Leu Leu Thr Phe His Ala Ala Pro Ala Gln Pro Gln Pro Ala Tyr Gly
100 105 110

Ser

<210> 167
<211> 248
<212> DNA
<213> Mus musculus

<400> 167
acatctctcg gaggaccatg ggctctggcg ggaagagagc cttcgagagg cggtagagat 60
tgccaagggt gaactggatg ctgggtgttg tgacgcgaag ctctgtggat ttggtggagc 120
tgtcctgagg gcagatgtca ctctcgctg agaatgggga cactgtgat gtattcttca 180
gctcataaag tggcaagttg tctgaaatgc cgccatccac atagcgcacc ccttagaggc 240
taggatcc 248

<210> 168
<211> 107
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (2)..(30)
<223> XAA = ANYTHING

<400> 168
Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Ser Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Leu Xaa Cys Xaa Xaa Ile Ser
20 25 30
Arg Arg Thr Met Gly Ser Gly Gly Lys Arg Ala Phe Glu Arg Arg Arg
35 40 45
Leu Arg Arg Leu Asn Trp Met Leu Val Leu Val Thr Arg Ser Ser Trp
50 55 60
Met Leu Val Glu Leu Ser Gly Gln Met Ser Leu Ser Pro Glu Asn Gly
65 70 75 80
Asp Thr Val Met Val Phe Phe Ser Ser Ser Gly Lys Leu Ser Glu Met
85 90 95
Pro Pro Ser Thr Arg Thr Pro Arg Leu Gly Ser
100 105

<210> 169
<211> 420
<212> DNA
<213> Mus musculus

<220>
 <221> modified_base
 <222> (46)..(63)
 <223> N = A, C, G OR T/U

<400> 169
 gaattcgcg cgcgctcgac cttttttttt tttttttttt tttttntttt tttttntn 60
 nnnnggatttt tccaagataa aactttattg gagacagcaa ggagtatact gaaagtgggg 120
 gagccatgcc ttcattccat aactgcaatc agatgctctc ctctgagaga gagtgtgtgg 180
 ggagccaagg tgagaagcag gtatgattca caccccaact gcttggagag tgcttatatg 240
 acagtctttt tctcgatttt attttttctc agttcttcaa cacacacttt ggcttcattt 300
 gggggaaaat taaacaaaag aacagaattt ccctcccca gagttactta tgaaatgaca 360
 cagctgccct tttctttgaa gggattcttg tcttctggga ttccctttac cagaggatcc 420

<210> 170
 <211> 140
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (16)..(21)
 <223> XAA = ANYTHING

<400> 170
 Glu Phe Ala Ala Ala Ser Thr Phe Phe Phe Phe Phe Phe Phe Phe Xaa
 1 5 10 15
 Phe Phe Phe Xaa Xaa Gly Phe Phe Gln Asp Lys Thr Leu Leu Glu Thr
 20 25 30
 Ala Arg Ser Ile Leu Lys Val Gly Glu Pro Cys Leu His Ser Ile Thr
 35 40 45
 Ala Ile Arg Cys Ser Pro Leu Arg Glu Ser Val Trp Gly Ala Lys Val
 50 55 60
 Arg Ser Arg Tyr Asp Ser His Pro Asn Cys Leu Glu Ser Ala Tyr Met
 65 70 75 80
 Thr Val Phe Phe Ser Ile Leu Phe Phe Leu Ser Ser Ser Thr His Thr
 85 90 95
 Leu Ala Ser Phe Gly Gly Lys Leu Asn Lys Arg Thr Glu Phe Pro Ser
 100 105 110
 Pro Arg Val Thr Tyr Glu Met Thr Gln Leu Pro Phe Ser Leu Lys Gly
 115 120 125
 Phe Leu Ser Ser Gly Ile Pro Phe Thr Arg Gly Ser
 130 135 140

<210> 171
 <211> 334
 <212> DNA
 <213> Mus musculus

<400> 171
 gaattcgcgg ccgcgtcgac ggcggctccg gaggtgctgg agtcagacgt gtcaagttcg 60
 ataacacttt tgaaaaacct ccaggagcag gtgagtatgt atgtctttta gaataaatca 120
 gtcagggggtt aactttgact ttgtaagtct catccacaca ctttgatgat tcgaataacta 180
 caaaattatc ttaggtgtaa aataaaagcc ttatatgcgc ttcattgaaag ttcaaaataa 240
 ttcattcagc tcccaaagaa atacagaaag ctgtttttcc cccattcact tacttattta 300
 tttattttat ttagtcactt tacattccgg atcc 334

<210> 172
 <211> 105
 <212> PRT
 <213> Mus musculus

<400> 172
 Asn Ser Arg Pro Arg Arg Arg Arg Leu Arg Arg Cys Trp Ser Gln Thr
 1 5 10 15
 Cys Gln Val Arg His Phe Lys Thr Ser Arg Ser Arg Val Cys Met Ser
 20 25 30
 Phe Arg Ile Asn Gln Ser Gly Val Asn Phe Asp Phe Val Ser Leu Ile
 35 40 45
 His Thr Leu Phe Glu Tyr Tyr Lys Ile Ile Leu Gly Val Lys Lys Pro
 50 55 60
 Tyr Met Arg Phe Met Lys Val Gln Asn Asn Ser Phe Ser Ser Gln Arg
 65 70 75 80
 Asn Thr Glu Ser Cys Phe Ser Pro Ile His Leu Leu Ile Tyr Leu Phe
 85 90 95
 Tyr Leu Val Thr Leu His Ser Gly Ser
 100 105

<210> 173
 <211> 648
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (11)..(43)
 <223> N = A, C, G OR T/U

<400> 173
 tccacagtac ntgcctntaga agccttggac ctgcctngtcc tcntaggcca cttcaggctc 60
 agatgctacc aatgttgtct ccttgaacag agtctgagcc ccttgccagc tccttcttcc 120

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atttcctagg agcattgtgg gtgtgccagt ggatggctgg ctgacgtgtg gatagactga 180
tgggtgtgtgt ctagatgggtg gtgggtgggta tatggatgat ggatggatgg gtgggtgggt 240
gaatggatga atggatgagt ggggtggtagg tatgtaattg ggtaaatgat ggatagatac 300
atatttaggg agaaatcttt ttctagagag tttgtttaaa aactagccaa gcttaggtgg 360
caaccggaac aaagatgggtc ccaagtgtag ggaggggtct gatgccttcc acgtggtttt 420
agctcttatt ttatgattga ttgttcagta attcctgcat taaccaagtg gagactgact 480
ttggaacaat ctaagtggat tattttagcg ggcttcctt tggctgggggt catgctggct 540
caggtgtgga ttaaccacag tcacttcctc tcagccttgc tggactgtgg tggacgggat 600
cttagcaggg tgaaggcagc ccagatgatg agagaggcga ggggatcc 648

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<210> 174
<211> 208
<212> PRT
<213> Mus musculus

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<220>
<221> MOD_RES
<222> (4)..(15)
<223> XAA = ANYTHING

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<400> 174
Ser Thr Val Xaa Ala Xaa Glu Ala Leu Asp Leu Pro Val Leu Xaa Gly
 1             5             10             15

His Phe Arg Leu Arg Cys Tyr Gln Cys Cys Leu Leu Glu Gln Ser Leu
      20             25             30

Ser Pro Leu Pro Ala Pro Ser Ser Ile Ser Glu His Cys Gly Cys Ala
      35             40             45

Ser Gly Trp Leu Ala Asp Val Trp Ile Asp Trp Cys Val Ser Arg Trp
      50             55             60

Trp Trp Trp Val Tyr Gly Trp Met Asp Gly Trp Val Gly Glu Trp Met
      65             70             75             80

Asn Gly Val Gly Gly Arg Tyr Val Ile Gly Met Met Asp Arg Tyr Ile
      85             90             95

Phe Arg Glu Lys Ser Phe Ser Arg Glu Phe Val Lys Leu Ala Lys Leu
      100            105            110

Arg Trp Gln Pro Glu Gln Arg Trp Ser Gln Val Gly Gly Val Cys Leu
      115            120            125

Pro Arg Gly Phe Ser Ser Tyr Phe Met Ile Asp Cys Ser Val Ile Pro
      130            135            140

Ala Leu Thr Lys Trp Arg Leu Thr Leu Glu Gln Ser Lys Trp Ile Ile
      145            150            155            160

Leu Ala Gly Phe Pro Leu Ala Gly Val Met Leu Ala Gln Val Trp Ile
      165            170            175

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Asn His Ser His Phe Leu Ser Ala Leu Leu Asp Cys Gly Gly Arg Asp
 180 185 190

Leu Ser Arg Val Lys Ala Ala Gln Met Met Arg Glu Ala Arg Gly Ser
 195 200 205

<210> 175
 <211> 619
 <212> DNA
 <213> Mus musculus

<400> 175
 gaagtgaag ttcgtccaag gcagcacaac tgcacttggtg tgttataaca gccagatcac 60
 agctccctat gcggaccgag tcaccttctc atccagtggc atcacgttca gttctgtgac 120
 ccggaaggac aatggagagt atacttgcag ggtctccgag gaaggtggcc agaactacgg 180
 ggaggtcagc atccacctca ctgtgcttgt acctccatcc aagccgacga tcagtgtccc 240
 ctctctgtgc accattggga acagggcagt gctgacctgc tcagagcatg atggttcccc 300
 acctctgaa tattcctggt tcaaggacgg gatatccatg cttacagcag atgccaagaa 360
 aacccgggcc ttcattgaatt cttcattcac cattgatcca aagtcggggg atctgatctt 420
 tgaccccggtg acagcctttg atagtgggtga atactactgc caggcccaga atggatatgg 480
 gacagccatg aggtcagagg ctgcacacat ggatgctgtg gagctgaatg tggggggcat 540
 cgtggcagct gtcttggtaa cactgattct ccttggaactc ttgatttttg gcgtctggtt 600
 tgcctatagc cacgcatcc 619

<210> 176
 <211> 205
 <212> PRT
 <213> Mus musculus

<400> 176
 Lys Lys Phe Val Gln Gly Ser Thr Thr Ala Leu Val Cys Tyr Asn Ser
 1 5 10 15
 Gln Ile Thr Ala Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Ser Gly
 20 25 30
 Ile Thr Phe Ser Ser Val Thr Arg Lys Asp Asn Gly Glu Tyr Thr Cys
 35 40 45
 Met Val Ser Glu Glu Gly Gly Gln Asn Tyr Gly Glu Val Ser Ile His
 50 55 60
 Leu Thr Val Leu Val Pro Pro Ser Lys Pro Thr Ile Ser Val Pro Ser
 65 70 75 80
 Ser Val Thr Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu His Asp
 85 90 95
 Gly Ser Pro Pro Ser Glu Tyr Ser Trp Phe Lys Asp Gly Ile Ser Met
 100 105 110

Leu Thr Ala Asp Ala Lys Lys Thr Arg Ala Phe Met Asn Ser Ser Phe
115 120 125

Thr Ile Asp Pro Lys Ser Gly Asp Leu Ile Phe Asp Pro Val Thr Ala
130 135 140

Phe Asp Ser Gly Glu Tyr Tyr Cys Gln Ala Gln Asn Gly Tyr Gly Thr
145 150 155 160

Ala Met Arg Ser Glu Ala Ala His Met Asp Ala Val Glu Leu Asn Val
165 170 175

Gly Gly Ile Val Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Leu
180 185 190

Leu Ile Phe Gly Val Trp Phe Ala Tyr Ser His Gly Ser
195 200 205

<210> 177

<211> 542

<212> DNA

<213> Mus musculus

<400> 177

gaattcgcgg ccgcgtcgac caagcccaga tgttgctgag catgaacagc ctggagtcgc 60
tgaatgcggg tgtacagcag aacaatactg agtcctttgc cgctcgtctc tgccatcttg 120
cagagctcca tgcagaacag ggctgttttg cggctgctgg tgaagtatta aagcacttga 180
aggaccgatt tccacccaac agtcagcacg cccagttatg gatgctgtgt gatcaaaaaa 240
tacagtttga cagagcaatg aatgatggca aattccattt ggctgattca cttgttacag 300
gaatcacagc gcttaatggc atagaagggtg tatacaggaa agcagtcgta ctgcaggctc 360
agaaccaa at gacagaggca cacaagctac tacagaagtt gctgacatac tgtcagaagt 420
taaagaacac agaaatgggtc atcagtggtcc tcctatcggt ggcagagctg tactggcgat 480
cttcgtcccc gaccatcgcc atgcctgtgc tcctggaagc tctggccctc tccaaaggat 540
cc 542

<210> 178

<211> 180

<212> PRT

<213> Mus musculus

<400> 178

Ile Arg Gly Arg Val Asp Gln Ala Gln Met Leu Leu Ser Met Asn Ser
1 5 10 15

Leu Glu Ser Leu Asn Ala Gly Val Gln Gln Asn Asn Thr Glu Ser Phe
20 25 30

Ala Val Ala Leu Cys His Leu Ala Glu Leu His Ala Glu Gln Gly Cys
35 40 45

Phe Ala Ala Ala Gly Glu Val Leu Lys His Leu Lys Asp Arg Phe Pro
50 55 60

Pro Asn Ser Gln His Ala Gln Leu Trp Met Leu Cys Asp Gln Lys Ile
65 70 75 80

Gln Phe Asp Arg Ala Met Asn Asp Gly Lys Phe His Leu Ala Asp Ser
85 90 95

Leu Val Thr Gly Ile Thr Ala Leu Asn Gly Ile Glu Gly Val Tyr Arg
100 105 110

Lys Ala Val Val Leu Gln Ala Gln Asn Gln Met Thr Glu Ala His Lys
115 120 125

Leu Leu Gln Lys Leu Leu Thr Tyr Cys Gln Lys Leu Lys Asn Thr Glu
130 135 140

Met Val Ile Ser Val Leu Leu Ser Val Ala Glu Leu Tyr Trp Arg Ser
145 150 155 160

Ser Ser Pro Thr Ile Ala Met Pro Val Leu Leu Glu Ala Leu Ala Leu
165 170 175

Ser Lys Gly Ser
180

<210> 179
<211> 640
<212> DNA
<213> Mus musculus

<400> 179
caagtcaatg tacaaaatgt ctggcaatgc ctcattttaa attaaattgg tttattgaga 60
acagctgttt ttgatgtgta acgtgaagca agacagagcc ctgctgtgag cagctggcag 120
aagatttttt ttttttaatt attggtacat attacccttc aaatctgaga atttggacta 180
attgcaccaa agaaccctct aatttgggtcc ctggcacatg cgtacctgtc aacttttttt 240
cttttacaag acctgcatgc tgtcggccat cgccttctcc aatgtttttg agcactattt 300
gggggatgac atgaaaaggg aaaaccacc tgtggaggac agcagtgatg aggatgacaa 360
aagaaaccca ggaaacttgt atgacaaggc aggtaaagtg aggaagcatg tgacagagca 420
agagaaacct gaagagggtc tgggccccaa catcaaaagc attgtgacca tgctgatgct 480
catgctcctg atgatgttcg cgggccactg cacgtgggtc acaagcaacg cctactccag 540
tccaagtgtg gtccttgctt cctacaatca tgatgggtacc aggaatatat tagatgattt 600
tagagaagcg tacttttggc tgagacaaaa caccggatcc 640

<210> 180
<211> 209
<212> PRT
<213> Mus musculus

<400> 180
Lys Ser Met Tyr Lys Met Ser Gly Asn Ala Ser Phe Lys Ile Lys Leu
1 5 10 15

Val Tyr Glu Gln Leu Phe Leu Met Cys Asn Val Lys Gln Asp Arg Ala

20	25	30
Leu Leu Ala Ala Gly Arg Arg Phe Phe Phe Phe Asn Tyr Trp Tyr Ile		
35	40	45
Leu Pro Phe Lys Ser Glu Asn Leu Asp Leu His Gln Arg Thr Leu Phe		
50	55	60
Gly Pro Trp His Met Arg Thr Cys Gln Leu Phe Phe Phe Tyr Lys Thr		
65	70	75
Cys Met Leu Ser Ala Ile Ala Phe Ser Asn Val Phe Glu His Tyr Leu		
85	90	95
Gly Asp Asp Met Lys Arg Glu Asn Pro Pro Val Glu Asp Ser Ser Asp		
100	105	110
Glu Asp Asp Lys Arg Asn Pro Gly Asn Leu Tyr Asp Lys Ala Gly Lys		
115	120	125
Val Arg Lys His Val Thr Glu Gln Glu Lys Pro Glu Glu Gly Leu Gly		
130	135	140
Pro Asn Ile Lys Ser Ile Val Thr Met Leu Met Leu Met Leu Leu Met		
145	150	155
Met Phe Ala Val His Cys Thr Trp Val Thr Ser Asn Ala Tyr Ser Ser		
165	170	175
Pro Ser Val Val Leu Ala Ser Tyr Asn His Asp Gly Thr Arg Asn Ile		
180	185	190
Leu Asp Asp Phe Arg Glu Ala Tyr Phe Trp Leu Arg Gln Asn Thr Gly		
195	200	205

Ser

<210> 181
 <211> 671
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (5)..(71)
 <223> N = A, C, G OR T/U

<400> 181
 agccngttta tctttgggta canaaagccc actgattggg ttgtgttatt ttatatcaag 60
 ctactgcact naagctgttt atctgggtta ggagttctct ggtgaatttt agggtcactt 120
 atatatacta tcatatcatc tgcaaatagt gatatttttg acttcttctt tccaatttgt 180
 atcccccttga cctccttttg ttgtggaatt gctctggcta ggacttcaag tactatattg 240
 aatagggtggg gagaaagtgg cagcttgtct agtccctgat tttagtggga ttgcttccag 300

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tttctatcca tttactttga tgttggtac tggtttgctg tagattgctt ttattatggt 360
caggatggg ccttgaattc ctgatctttc caagactttt atcttgaatg ggtgttggtat 420
tttgtcaaat gctttttccg catctaata tcatgtgggt tttgtctttg agtttgcttt 480
tatagtggat tacaatgatg gatttccgta tattaaccca tccctgcatc cctgggatga 540
agtctacttg gtcagtatgg atgatcattt tgatgtgttc ttggatttgg tttgctagga 600
ttttattgag tatttttgca ttgatattca taagggaat tggctgaag ttctctatcc 660
ttgttggtac c 671

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<210> 182
<211> 212
<212> PRT
<213> Mus musculus

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<220>
<221> MOD_RES
<222> (7)
<223> XAA = ANYTHING

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<400> 182
Pro Val Tyr Leu Trp Val Xaa Lys Ala His Leu Val Cys Val Ile Leu
  1             5             10             15
Tyr Gln Ala Thr Ala Leu Lys Leu Phe Ile Trp Phe Arg Ser Ser Leu
             20             25             30
Val Asn Phe Arg Val Thr Tyr Ile Tyr Tyr His Ile Ile Cys Lys Tyr
             35             40             45
Phe Leu Leu Leu Ser Asn Leu Tyr Pro Leu Asp Leu Leu Leu Leu Trp
             50             55             60
Asn Cys Ser Gly Asp Phe Lys Tyr Tyr Ile Glu Val Gly Arg Lys Trp
             65             70             75             80
Gln Leu Val Ser Leu Ile Leu Val Gly Leu Leu Pro Val Ser Ile His
             85             90             95
Leu Leu Cys Trp Leu Leu Val Cys Cys Arg Leu Leu Leu Leu Cys Ser
             100            105            110
Gly Met Gly Leu Glu Phe Leu Ile Phe Pro Arg Leu Leu Ser Met Gly
             115            120            125
Val Gly Phe Cys Gln Met Leu Phe Pro His Leu Met Ile Met Trp Phe
             130            135            140
Leu Ser Leu Ser Leu Leu Leu Trp Ile Thr Met Met Asp Phe Arg Ile
             145            150            155            160
Leu Asn His Pro Cys Ile Pro Gly Met Lys Ser Thr Trp Ser Trp Met
             165            170            175
Ile Ile Leu Met Cys Ser Trp Ile Trp Phe Ala Arg Ile Leu Leu Ser
             180            185            190

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Ile Phe Ala Leu Ile Phe Ile Arg Glu Ile Gly Leu Lys Phe Ser Ile
 195 200 205

Leu Val Gly Ser
 210

<210> 183

<211> 637

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (23)..(98)

<223> N = A, C, G OR T/U

<400> 183

aagtcaatgt acaaaatgtc tgncaatgcn tcatttataaa tttaaattggt ttattgagac 60
 agctgtttnt gatgtgtaac gtgaagcaag acagagccnt gttgtgagca gtggcagaag 120
 attttttttt tttaattatt ggtacatatt acccttcaaa tctgagaatt tggactaatt 180
 gcaccaaaga accctctaata ttggtccctg gcacatgcgt acctgtcaac tttttttctt 240
 ttacaagacc tgcattgctgt cggccatcgc cttctccaat gtttttgagc actatttggg 300
 ggatgacatg aaaagggaaa acccacctgt ggaggacagc agtgatgagg atgacaaaag 360
 aaacccagga aacttgatg acaaggcagg taaagtgagg aagcatgtga cagagcaaga 420
 gaaacctgaa gagggcttgg gccccaacat caaaagcatt gtgacctgc tgatgctcat 480
 gctcctgatg atgttcgcgg tccactgcac gtgggtcaca agcaacgcct actccagtcc 540
 aagtgtggtc cttgcctcct acaatcatga tggtagcagg aatatattag atgattttag 600
 agaagcgtac ttttggctga gacaaaacac cggatcc 637

<210> 184

<211> 209

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (8)..(32)

<223> XAA = ANYTHING

<400> 184

Ser Gln Cys Thr Lys Cys Leu Xaa Met Xaa His Leu Lys Leu Asn Trp
 1 5 10 15

Phe Ile Glu Thr Ala Val Xaa Asp Val Arg Glu Ala Arg Gln Ser Xaa
 20 25 30

Val Val Ser Ser Gly Arg Arg Phe Phe Phe Asn Tyr Trp Tyr Ile
 35 40 45

Leu Pro Phe Lys Ser Glu Asn Leu Asp Leu His Gln Arg Thr Leu Phe
 50 55 60

Gly Pro Trp His Met Arg Thr Cys Gln Leu Phe Phe Phe Tyr Lys Thr
 65 70 75 80
 Cys Met Leu Ser Ala Ile Ala Phe Ser Asn Val Phe Glu His Tyr Leu
 85 90 95
 Gly Asp Asp Met Lys Arg Glu Asn Pro Pro Val Glu Asp Ser Ser Asp
 100 105 110
 Glu Asp Asp Lys Arg Asn Pro Gly Asn Leu Tyr Asp Lys Ala Gly Lys
 115 120 125
 Val Arg Lys His Val Thr Glu Gln Glu Lys Pro Glu Glu Gly Leu Gly
 130 135 140
 Pro Asn Ile Lys Ser Ile Val Thr Met Leu Met Leu Met Leu Leu Met
 145 150 155 160
 Met Phe Ala Val His Cys Thr Trp Val Thr Ser Asn Ala Tyr Ser Ser
 165 170 175
 Pro Ser Val Val Leu Ala Ser Tyr Asn His Asp Gly Thr Arg Asn Ile
 180 185 190
 Leu Asp Asp Phe Arg Glu Ala Tyr Phe Trp Leu Arg Gln Asn Thr Gly
 195 200 205
 Ser

<210> 185

<211> 669

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (8)..(119)

<223> N = A, C, G OR T/U

<400> 185

cgccccancc aanctgttcg ccaggctaaa ggcgcgcatg ccgacggcga gnatctcgtc 60
 gtgacccatg ccgatgcntg cttgccnaat atcatgggtga aaatggccgc tttttctgna 120
 ttcacgcact gtggccggct ggggtgtggcg gaccgctatc aggacatagc gttggctacc 180
 cgtgatattg ctaagagctt ggcggcgaat gggctgaccg cttcctcgctg ctttacggta 240
 tcgccgctcc cgattcgcag cgcacgcct tctatcgctt tcttgacgag ttcttctgaa 300
 ttgaaaaaga agagtaagct tgaattcgcg gccgcgtcga ccgcggtac aacctccgga 360
 gcgatgcccg tggggggcct gttgccgctc ttcagtagcc ctggggggcg cggcctgggc 420
 agtggcctgg gcggggggct tggcggcggg aggaaggggt ctggccccgc tgccttcgcg 480
 ctcaccgaga agttcgtgct gctgctgggt ttcagcgcct tcatcacgct ctgcttcggg 540
 gcaatcttct tctgacctga ctctccaag ctgctcagcg gggctcctgtt ccaactccaac 600
 cctgccttgc agccgccggc ggagcacaag cccgggctcg gggcgcgctgc ggaggatgcc 660
 gccgatcc 669

<210> 186
 <211> 223
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (5)..(40)
 <223> XAA = ANYTHING

<400> 186
 Arg Pro Xaa Gln Xaa Val Arg Gln Ala Lys Gly Ala His Ala Asp Gly
 1 5 10 15
 Glu Xaa Leu Val Val Thr His Ala Asp Ala Cys Leu Pro Asn Ile Met
 20 25 30
 Val Lys Met Ala Ala Phe Ser Xaa Phe Ile Asp Cys Gly Arg Leu Gly
 35 40 45
 Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala Thr Arg Asp Ile Ala
 50 55 60
 Lys Ser Leu Ala Ala Asn Gly Leu Thr Ala Ser Ser Cys Phe Thr Val
 65 70 75 80
 Ser Pro Leu Pro Ile Arg Ser Ala Ser Pro Ser Ile Ala Phe Leu Thr
 85 90 95
 Ser Ser Ser Glu Leu Lys Lys Lys Ser Lys Leu Glu Phe Ala Ala Ala
 100 105 110
 Ser Thr Ala Ala Thr Thr Ser Gly Ala Met Pro Val Gly Gly Leu Leu
 115 120 125
 Pro Leu Phe Ser Ser Pro Gly Gly Gly Gly Leu Gly Ser Gly Leu Gly
 130 135 140
 Gly Gly Leu Gly Gly Gly Arg Lys Gly Ser Gly Pro Ala Ala Phe Arg
 145 150 155 160
 Leu Thr Glu Lys Phe Val Leu Leu Leu Val Phe Ser Ala Phe Ile Thr
 165 170 175
 Leu Cys Phe Gly Ala Ile Phe Phe Leu Pro Asp Ser Ser Lys Leu Leu
 180 185 190
 Ser Gly Val Leu Phe His Ser Asn Pro Ala Leu Gln Pro Pro Ala Glu
 195 200 205
 His Lys Pro Gly Leu Gly Ala Arg Ala Glu Asp Ala Ala Gly Ser
 210 215 220

<210> 187
 <211> 280
 <212> DNA
 <213> Mus musculus

<400> 187
 gaattcgcgg ccgcgtcgac ctcagcttga tctactggac ttgatttgga aaaaaaagtt 60
 ataactttca acaccaactt aaaatgtaat ttccttattt cataaggtgg gggaactgaa 120
 attcatgac tagaaggagc ttaaggtatt atctaggat agttcctccc ttttggggtt 180
 gattcttata atactttctg taattttctc tataaatatt aatatgtatt tattgtgtgt 240
 gggatatcat atatatgtat gtatatatga atatggatcc 280

<210> 188
 <211> 217
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (3)..(37)
 <223> XAA = ANYTHING

<400> 188
 His Val Xaa Gly Asn Arg Ser Cys Arg Xaa Gly Xaa Gly Arg Xaa Ser
 1 5 10 15
 Ile Arg Gly Ser Arg Pro Pro Xaa Leu Phe Ala Arg Xaa Lys Ala Arg
 20 25 30
 His Ala Arg Arg Xaa Arg Ser Ser Ser Val Thr His Gly Asp Ala Cys
 35 40 45
 Leu Pro Asn Ile Met Val Lys Met Ala Ala Phe Leu Asn Ser Ser Thr
 50 55 60
 Val Ala Gly Trp Val Trp Arg Pro Leu Ser Asp Ile Ala Leu Ala Thr
 65 70 75 80
 Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu
 85 90 95
 Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr
 100 105 110
 Arg Leu Leu Asp Glu Phe Phe Ile Glu Lys Gly Arg Val Ser Leu Asn
 115 120 125
 Ser Arg Pro Arg Arg Pro Gln Leu Asp Leu Leu Asp Leu Ile Trp Lys
 130 135 140
 Lys Lys Leu Leu Ser Thr Pro Thr Asn Val Ile Ser Leu Phe His Lys
 145 150 155 160
 Val Gly Glu Leu Lys Phe Met Ile Lys Glu Leu Lys Val Leu Ser Arg

Phe Gln Gln Ile Phe Pro Leu Cys Ser Leu Trp Thr Gly Tyr Leu Phe
 115 120 125

Ile Tyr Phe Leu Phe Cys Ser Asp Val Leu Thr Pro Tyr Ala Trp Lys
 130 135 140

Val Leu Gly Ser
 145

<210> 191
 <211> 289
 <212> DNA
 <213> Mus musculus

<400> 191
 gaattcgcg cgcgctcgac gccaaagactt cacacagttc tgattgtccc agaagccttg 60
 cgtttgtcaa aacatgacaa tgagatatga aaacttccag aacttggagc gggaagagaa 120
 aaaccaggag atgagaaatg gtgacaagaa aggaggaatg gagtctccaa agtttgctct 180
 aattccttcc cagtccttcc tgtggcgcat cctctcttgg acccacctcc tcctgttctc 240
 cctgggcctc agcctcctgc tactggtggt catctccgtg attggatcc 289

<210> 192
 <211> 95
 <212> PRT
 <213> Mus musculus

<400> 192
 Asn Ser Arg Pro Arg Arg Arg Gln Asp Phe Thr Gln Phe Leu Ser Gln
 1 5 10 15

Lys Pro Cys Val Cys Gln Asn Met Thr Met Arg Tyr Glu Asn Phe Gln
 20 25 30

Asn Leu Glu Arg Glu Glu Lys Asn Gln Glu Met Arg Asn Gly Asp Lys
 35 40 45

Lys Gly Gly Met Glu Ser Pro Lys Phe Ala Leu Ile Pro Ser Gln Ser
 50 55 60

Phe Leu Trp Arg Ile Leu Ser Trp Thr His Leu Leu Leu Phe Ser Leu
 65 70 75 80

Gly Leu Ser Leu Leu Leu Leu Val Val Ile Ser Val Ile Gly Ser
 85 90 95

<210> 193
 <211> 658
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base

<222> (24) .. (152)

<223> N = A, C, G OR T/U

<400> 193

aaactgacgg catgatgagg acantatgac gaaagtaaag gttacaaaaan gagctgagaa 60
cagctgggtc cagtgcgaag anacacggcc aggttggcaa anaggtgcag cggcacaggc 120
cgactcgnag ccgacatgaa ggatctacgc anccgactcg ggcagtaccg caacgaggtg 180
cacaccatgt tgggccagag cacagaggag atacggggcg ggctctccac acacctgcgc 240
aagatgcgca agcgcttgat gcgggatgcc gaggatctgc agaagcgcct agcttggtgta 300
caaggcaggg gcacgcgagg gcgccgagcg cgggtgtgagt gccatccgtg agcgctggg 360
gcctctggtg gagcaaggct gccagcgcac cgccaaccta ggcgctgggg ccgcccagcc 420
tctgcgcgat cgcgcccagg cttttggtga ccgcatccga gggcggctgg aggaagtggg 480
caaccaggcc cgtgaccgcc tagaggaggt gcgtgagcac atggaggagg tgcgctccaa 540
gatggaggaa ctctcgagtc ccagcatcag agcgcgtgga ccttttcccg cgtcccgcag 600
catgcaggtc tcccgtgtgc tggccgcgct gtgcggcatg ctactctgcg ccggatcc 658

<210> 194

<211> 215

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (7) .. (49)

<223> XAA = ANYTHING

<400> 194

Asn Arg His Asp Glu Asp Xaa Met Thr Lys Val Lys Val Thr Lys Xaa
1 5 10 15

Ala Glu Asn Ser Trp Val Gln Cys Glu Xaa Thr Arg Pro Gly Trp Gln
20 25 30

Xaa Gly Ala Ala Ala Gln Ala Asp Ser Xaa Pro Thr Arg Ile Tyr Ala
35 40 45

Xaa Asp Ser Gly Ser Thr Ala Thr Arg Cys Thr Pro Cys Trp Ala Arg
50 55 60

Ala Gln Arg Arg Tyr Gly Arg Gly Ser Pro His Thr Cys Ala Arg Cys
65 70 75 80

Ala Ser Ala Cys Gly Met Pro Arg Ile Cys Arg Ser Ala Leu Val Tyr
85 90 95

Lys Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Val Ser Ala Ile Arg
100 105 110

Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Gln Arg Thr Ala Asn
115 120 125

Leu Gly Ala Gly Ala Ala Gln Pro Leu Arg Asp Arg Ala Gln Ala Phe
130 135 140

Gly Asp Arg Ile Arg Gly Arg Leu Glu Glu Val Gly Asn Gln Ala Arg
 145 150 155 160

Asp Arg Leu Glu Glu Val Arg Glu His Met Glu Glu Val Arg Ser Lys
 165 170 175

Met Glu Glu Leu Ser Ser Pro Ser Ile Arg Ala Arg Gly Pro Phe Pro
 180 185 190

Ala Ser Arg Ser Met Gln Val Ser Arg Val Leu Ala Ala Leu Cys Gly
 195 200 205

Met Leu Leu Cys Ala Gly Ser
 210 215

<210> 195

<211> 412

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (14)

<223> N = A, C, G OR T/U

<400> 195

gaattcgcgg ccgnggcgac cttttttttt tttttttttt tttttttttt tttttttttt 60
 tttccaagat aaaactttat tggagacagc aaggagtata ctgaaagtgg gggagccatg 120
 ccttcattcc ataactgcaa tcagatgctc tctctgaga gagagtgtgt ggggagccaa 180
 ggtgagaagc aggtatgatt cacaccccaa ctgcttgagg agtgcttata tgacagtctt 240
 tttctcgatt ttattttttt tcagttcttc aacacacact ttggcttcat ttgggggaaa 300
 attaaacaaa agaacagaat ttccctcccc cagagttact tatgaaatga cacagctgcc 360
 cttttctttg aagggattct tgtcttctgg gattcccttt accagaggat cc 412

<210> 196

<211> 670

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (43)..(107)

<223> N = A, C, G, OR T/U

<400> 196

acaagcccta gccttggtgc atggcttcaa tttggacatt gancatccca tgaanttcca 60
 agagaatgca aaagnctttg nacagagtgt ggtccagctt ggcggancca gtgtggttgt 120
 tgcagccccc cagaaggcaa aggctgttaa ccagacaggt gccctctacc agtgtgacta 180
 cagcacaagc cgggtgtgacc ccatccccct gcaagtacct ccagaggctg tgaatatgtc 240
 cttgggcctg tccctggctg tttctactgt cccccagcag ctgctggcct gtggccccac 300
 ggtgcaccaa aactgcaagg agaatactta tgtgaatgga ttgtgctatt tggtcggctc 360
 caacctgctg aggcgcgccc agcagttccc agaggctctc agagaatgtc ctcagcagga 420
 gagtgcacatt gtcttcttga ttgatggctc cggtagcatc aacaacattg actttcagaa 480

gatgaaggag tttgtctcaa ctgtgatgga gcagttcaaa aagtctaaaa ccttggtctc 540
 tttgatgcag tactcggacg agttccggat tcacttcacc ttcaatgact tcaagagaaa 600
 ccctagccca agatcacacg tgagcccat aaagcagctg aatgggagga caaaaactgc 660
 ctcgggatcc 670

<210> 197
 <211> 223
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (14)..(36)
 <223> XAA = ANYTHING

<400> 197
 Gln Ala Leu Ala Leu Cys His Gly Phe Asn Leu Asp Ile Xaa His Pro
 1 5 10 15
 Met Thr Phe Gln Glu Asn Ala Lys Xaa Phe Xaa Gln Ser Val Val Gln
 20 25 30
 Leu Gly Gly Xaa Ser Val Val Val Ala Ala Pro Gln Lys Ala Lys Ala
 35 40 45
 Val Asn Gln Thr Gly Ala Leu Tyr Gln Cys Asp Tyr Ser Thr Ser Arg
 50 55 60
 Cys Asp Pro Ile Pro Leu Gln Val Pro Pro Glu Ala Val Asn Met Ser
 65 70 75 80
 Leu Gly Leu Ser Leu Ala Val Ser Thr Val Pro Gln Gln Leu Leu Ala
 85 90 95
 Cys Gly Pro Thr Val His Gln Asn Cys Lys Glu Asn Thr Tyr Val Asn
 100 105 110
 Gly Leu Cys Tyr Leu Phe Gly Ser Asn Leu Leu Arg Pro Pro Gln Gln
 115 120 125
 Phe Pro Glu Ala Leu Arg Glu Cys Pro Gln Gln Glu Ser Asp Ile Val
 130 135 140
 Phe Leu Ile Asp Gly Ser Gly Ser Ile Asn Asn Ile Asp Phe Gln Lys
 145 150 155 160
 Met Lys Glu Phe Val Ser Thr Val Met Glu Gln Phe Lys Lys Ser Lys
 165 170 175
 Thr Leu Phe Ser Leu Met Gln Tyr Ser Asp Glu Phe Arg Ile His Phe
 180 185 190
 Thr Phe Asn Asp Phe Lys Arg Asn Pro Ser Pro Arg Ser His Val Ser
 195 200 205

Pro Ile Lys Gln Leu Asn Gly Arg Thr Lys Thr Ala Ser Gly Ser
 210 215 220

<210> 198
 <211> 640
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (21)
 <223> N = A, C, G OR T/U

<400> 198
 ctgttgatgg cttttacatg nacgcctatg aagtcagcaa tgcggatttt gagaagtttg 60
 tgaactcgac tggctatttg acagagctga gaagtttgaa gactctttcg tctttgaagg 120
 catgttgagc gagcaagtga aaacgcatat ccaccaggca gttgcagctg ctccatgggtg 180
 gttgcctgtc aagggagcta attggagaca cccagagggt ccggactcca gtattctgca 240
 caggtcaaat catccggttc tccatgtttc ctggaacgat gctgttgctt actgcacatg 300
 ggcgggcaag aggttgacct ctgaggcaga gtgggaatac agctgtagag gaggcctgca 360
 gaacaggctt tccccctggg gcaacaaact gcagcccaaa ggacagcatt atgccaacat 420
 ctggcagggc aagtttctctg tgagcaaacac tggcgaggat ggcttccaag gaactgcccc 480
 cgttgatgcc tttcctccca atggctatgg cttatacaac atagtgggga atgtgtggga 540
 gtggacctca gactgggtga ctgttcacca ttctgttgag gaaacgttca acccaaaggg 600
 tcccacttct gggaaagacc gagtgaagaa ggggtggatcc 640

<210> 199
 <211> 210
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (6)
 <223> XAA = ANYTHING

<400> 199
 Cys Trp Leu Leu His Xaa Arg Leu Ser Gln Gln Cys Gly Phe Glu Val
 1 5 10 15
 Cys Glu Leu Asp Trp Leu Phe Asp Arg Ala Glu Lys Phe Glu Asp Ser
 20 25 30
 Phe Val Phe Glu Gly Met Leu Ser Glu Gln Val Lys Thr His Ile His
 35 40 45
 Gln Ala Val Ala Ala Ala Pro Trp Trp Leu Pro Val Lys Gly Ala Asn
 50 55 60
 Trp Arg His Pro Glu Gly Pro Asp Ser Ser Ile Leu His Arg Ser Asn
 65 70 75 80

His Pro Val Leu His Val Ser Trp Asn Asp Ala Val Ala Tyr Cys Thr
 85 90 95
 Trp Ala Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ser Cys
 100 105 110
 Arg Gly Gly Leu Gln Asn Arg Leu Phe Pro Trp Gly Asn Lys Leu Gln
 115 120 125
 Pro Lys Gly Gln His Tyr Ala Asn Ile Trp Gln Gly Lys Phe Pro Val
 130 135 140
 Ser Asn Thr Gly Glu Asp Gly Phe Gln Gly Thr Ala Pro Val Asp Ala
 145 150 155 160
 Phe Pro Pro Asn Gly Tyr Gly Leu Tyr Asn Ile Val Gly Asn Val Trp
 165 170 175
 Glu Trp Thr Ser Asp Trp Trp Thr Val His His Ser Val Glu Glu Thr
 180 185 190
 Phe Asn Pro Lys Gly Pro Thr Ser Gly Lys Asp Arg Val Lys Lys Gly
 195 200 205
 Gly Ser
 210

<210> 200
 <211> 263
 <212> DNA
 <213> Mus musculus

<400> 200
 gaattcgcg ggcgcgtcgac ggccagcctg gtctacagag tggattcctg tcctgtcagg 60
 gctgcacgat gagtccctat ctcaaagaag aagaaaaaaa aaaaagaaag aaagaaagac 120
 ttctttttga aatattagac aaccaatatg acaaaatagc aatgccaaac atcctgtgtg 180
 accgtacgat ctatttttgt tttttttttt ggttgttgtt cttgaccaa ataaatgatt 240
 accggaggga atcacatgga tcc 263

<210> 201
 <211> 87
 <212> PRT
 <213> Mus musculus

<400> 201
 Ile Arg Gly Arg Val Asp Gly Gln Pro Gly Leu Gln Ser Gly Phe Leu
 1 5 10 15
 Ser Cys Gln Gly Cys Thr Met Ser Pro Tyr Leu Lys Glu Glu Glu Lys
 20 25 30
 Lys Lys Arg Lys Lys Glu Arg Leu Leu Phe Glu Ile Leu Asp Asn Gln
 35 40 45

Tyr Asp Lys Ile Arg Met Pro Asn Ile Leu Leu Tyr Arg Thr Ile Tyr
 50 55 60

Phe Cys Phe Phe Phe Trp Leu Leu Phe Leu Thr Lys Ile Asn Asp Tyr
 65 70 75 80

Arg Arg Gln Ser His Gly Ser
 85

<210> 202
 <211> 544
 <212> DNA
 <213> Mus musculus

<400> 202
 gaattcgcgg ccgcgtcgac ctgtacgatt gtcagtggat ctgacgacac caaaagggct 60
 caggatgcta ctgttgcaag ctctcctggt cctcttaatc ctgcccagtc atgccgaaga 120
 tgacgttact acaactgaag agctagctcc tgccttggtc cctccacca agggaacttg 180
 tgcaggttgg atggcaggca tcccaggaca tccctggccac aatggcacac caggccgtga 240
 tggcagagat ggcactcctg gagagaaggg agagaaagga gatgcaggtc ttcttggtcc 300
 taagggtgag acaggagatg ttggaatgac aggagctgaa gggccacggg gcttccccgg 360
 aaccctggc aggaaaggag agcctggaga agccgcttat gtgtatcgct cagcgttcag 420
 tgtggggctg gagaccgcg tcaactgttcc caatgtaccc attcgcttta ctaagatctt 480
 ctacaaccaa cagaatcatt atgacggcag cactggcaag ttctactgca acattccagg 540
 atcc 544

<210> 203
 <211> 181
 <212> PRT
 <213> Mus musculus

<400> 203
 Asn Ser Arg Pro Arg Arg Pro Val Arg Leu Ser Val Asp Leu Thr Thr
 1 5 10 15

Pro Lys Gly Leu Arg Met Leu Leu Leu Gln Ala Leu Leu Phe Leu Leu
 20 25 30

Ile Leu Pro Ser His Ala Glu Asp Asp Val Thr Thr Thr Glu Glu Leu
 35 40 45

Ala Pro Ala Leu Val Pro Pro Pro Lys Gly Thr Cys Ala Gly Trp Met
 50 55 60

Ala Gly Ile Pro Gly His Pro Gly His Asn Gly Thr Pro Gly Arg Asp
 65 70 75 80

Gly Arg Asp Gly Thr Pro Gly Glu Lys Gly Glu Lys Gly Asp Ala Gly
 85 90 95

Leu Leu Gly Pro Lys Gly Glu Thr Gly Asp Val Gly Met Thr Gly Ala
 100 105 110

Glu Gly Pro Arg Gly Phe Pro Gly Thr Pro Gly Arg Lys Gly Glu Pro
115 120 125

Gly Glu Ala Ala Tyr Val Tyr Arg Ser Ala Phe Ser Val Gly Leu Glu
130 135 140

Thr Arg Val Thr Val Pro Asn Val Pro Ile Arg Phe Thr Lys Ile Phe
145 150 155 160

Tyr Asn Gln Gln Asn His Tyr Asp Gly Ser Thr Gly Lys Phe Tyr Cys
165 170 175

Asn Ile Pro Gly Ser
180

<210> 204

<211> 244

<212> DNA

<213> Mus musculus

<400> 204

gaattcgcgg ccgcgctcgac cattatTTTT ggttggttgt cttggggttag cattaaagcc 60
ttcacctatt tatggagggt taggtttaat tgtagtgagg tttggttggt gtttaatggt 120
tttaggggtt ggtggatcgt ttttaggttt aatagttttt ttaatttatt taggggggat 180
gttggttggt tttggatata cgactgctat agctactgag gaatatccag agacttggtg 240
atcc 244

<210> 205

<211> 81

<212> PRT

<213> Mus musculus

<400> 205

Asn Ser Arg Pro Arg Arg Pro Leu Phe Leu Val Gly Cys Leu Gly Leu
1 5 10 15

Ala Leu Lys Pro Ser Pro Ile Tyr Gly Gly Leu Gly Leu Ile Val Ser
20 25 30

Gly Phe Val Gly Cys Leu Met Val Leu Gly Phe Gly Gly Ser Phe Leu
35 40 45

Gly Leu Ile Val Phe Leu Ile Tyr Leu Gly Gly Met Leu Val Val Phe
50 55 60

Gly Tyr Thr Thr Ala Ile Ala Thr Glu Glu Tyr Pro Glu Thr Cys Gly
65 70 75 80

Ser

<210> 206
 <211> 244
 <212> DNA
 <213> Mus musculus

<400> 206
 gaattcgcgg ccgcgtcgac cattatTTTT ggttggttgt cttggggttag cattaaagcc 60
 ttcacctatt tatggaggtt taggtTTaat tgtagtggg tttggttggt gTTaatggt 120
 tttagggttt ggtggatcgt ttttaggttt aatagTTTT ttaatttatt taggggggat 180
 gttggttgtg tttgatata cgactgctat agctactgag gaatatccag agacttgtgg 240
 atcc 244

<210> 207
 <211> 81
 <212> PRT
 <213> Mus musculus

<400> 207
 Asn Ser Arg Pro Arg Arg Pro Leu Phe Leu Val Gly Cys Leu Gly Leu
 1 5 10 15
 Ala Leu Lys Pro Ser Pro Ile Tyr Gly Gly Leu Gly Leu Ile Val Ser
 20 25 30
 Gly Phe Val Gly Cys Leu Met Val Leu Gly Phe Gly Gly Ser Phe Leu
 35 40 45
 Gly Leu Ile Val Phe Leu Ile Tyr Leu Gly Gly Met Leu Val Val Phe
 50 55 60
 Gly Tyr Thr Thr Ala Ile Ala Thr Glu Glu Tyr Pro Glu Thr Cys Gly
 65 70 75 80
 Ser

<210> 208
 <211> 235
 <212> DNA
 <213> Mus musculus

<400> 208
 gaattcgcgg ccgcgtcgac ctagtgtgct ctttgagatt tTTaagagca tttgagatac 60
 aagaattttg aggggatgag gaatgttggT caaggTctaa atcacacata aaaaattttc 120
 ttctgtgaat ttatcttctt tgcataata tccctgctgg ccccttggtt tgattttggt 180
 attggtcatt ccagctctca gtggaagacc ggaccctgtc attcatgaag gatcc 235

<210> 209
 <211> 675
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (81)..(267)
 <223> N = A, C, G OR T/U

<400> 209
 gaattcgcg ccgctgcgac ccacgttttt tgaccacaaa ccgcaagttt tagatcctcg 60
 cgagtaggaa atgaaggggt nccacacaga aggcagcgcc cactgggctc cactgatgca 120
 gggtgcccac cagaccacat cactctggcc ctgggctcag ggcagtgatg gagtggtgaga 180
 gctttggccc gggtgccatt aagactcact ccaggtcaca ctgagggcaa ggggtgctag 240
 tccctggccg ctgggactct ctcactntga gttctcccat caccatcact aagaatgttt 300
 ttctggtaac cgaagttgaa ttgagacatc caaggtcatc tatgcatttg gacaagattc 360
 agacatctag gcggtctgtc cggctttacc ggggagaatc taaaaaagaa gcacattcat 420
 cctccattat tttgatgtca tatctaagac aaaatgtcaa taaatgaagt atcaacattc 480
 tatatcataa aagaagatac aattgcaatg ggaggtgcac aaataatgct tggcctaatt 540
 cacaatgcac tggggactct ctggctctct ttgcacaatc tagaagacaa gagatatagc 600
 atcgccata aacttatgtt agctagtatc tgctacctgt ttgtgtctgg aacatttttc 660
 atcaactcag gatcc 675

<210> 210
 <211> 218
 <212> PRT
 <213> Mus musculus

<400> 210
 Glu Phe Ala Ala Ser Thr His Val Phe Pro Thr Thr Ala Ser Phe
 1 5 10 15
 Arg Ser Ser Arg Val Gly Asn Glu Gly Val Pro His Arg Arg Gln Arg
 20 25 30
 Pro Leu Gly Ser Thr Asp Ala Gly Cys Pro Pro Asp His Ile Thr Leu
 35 40 45
 Ala Leu Gly Ser Gly His Asp Val Ser Val Arg Ala Leu Ala Arg Leu
 50 55 60
 Pro Leu Arg Leu Thr Pro Gly His Thr Glu Gly Lys Gly Cys Ser Leu
 65 70 75 80
 Ala Ala Gly Thr Leu Ser Ser Val Leu Pro Ser Pro Ser Leu Arg Met
 85 90 95
 Phe Phe Trp Pro Lys Leu Asn Asp Ile Gln Gly His Leu Cys Ile Trp
 100 105 110
 Thr Arg Phe Arg His Leu Gly Gly Leu Ser Gly Phe Thr Gly Glu Asn
 115 120 125
 Leu Lys Lys Lys His Ile His Pro Pro Leu Phe Cys His Ile Asp Lys
 130 135 140
 Met Ser Ile Asn Glu Val Ser Thr Phe Tyr Ile Ile Lys Glu Asp Thr
 145 150 155 160

Ile Ala Met Gly Gly Ala Gln Ile Met Leu Gly Leu Ile His Asn Ala
165 170 175

Leu Gly Thr Leu Trp Leu Ser Leu His Asn Leu Glu Asp Lys Arg Tyr
180 185 190

Ser Ile Gly His Lys Leu Met Leu Ala Ser Ile Cys Tyr Leu Phe Val
195 200 205

Ser Gly Thr Phe Phe Ile Asn Ser Gly Ser
210 215

<210> 211

<211> 630

<212> DNA

<213> Mus musculus

<400> 211

gaattcgcgg cccgcgtcga cgtcactgtg gagctcagat cacagtgtctg acagaatcca 60
tatttggaga attacataag gtttgaaaga gaggatagtg aaaggatacg aattcctaaa 120
aacgtttaat ctggcctttt gtttgaacga aagagaaatt gaaaccaaatt gaaataaatt 180
acttgtaga agaataactg ccaacagcat agcaaaatga aattcttcct gctgctttcc 240
ctcattggat tctgctgggc ccaatatgac ccacatactc aatatggacg aactgctatt 300
gtccacctgt ttgagtggcg ctgggttgat attgctaagg aatgtgagag atacttagct 360
cctaattgat ttgcaggtgt gcaggtctct ccacccaatg aaaacatcgt agtccacagc 420
ccttcaagac catggtggga aagatatcaa ccaattagct acaaaatatg ttccaggtct 480
ggaaatgaag atgaattcag ggacatggtg aacaggtgca acaatgttgg tgtccgtatt 540
tatgtggatg ctgtcattaa ccacatgtgt ggagtggggg ctcaagctgg acaaagcagt 600
acatgtggaa gttatttcaa ccccggtacc 630

<210> 212

<211> 205

<212> PRT

<213> Mus musculus

<400> 212

Glu Phe Ala Ala Arg Val Asp Val Thr Val Glu Leu Arg Ser Gln Cys
1 5 10 15

Gln Asn Pro Tyr Leu Glu Asn Tyr Ile Arg Phe Glu Arg Glu Asp Ser
20 25 30

Glu Arg Ile Arg Ile Pro Lys Asn Val Ser Gly Leu Leu Phe Glu Arg
35 40 45

Lys Arg Asn Asn Gln Met Lys Ile Thr Cys Lys Glu Tyr Cys Gln Gln
50 55 60

His Ser Lys Met Lys Phe Phe Leu Leu Leu Ser Leu Ile Gly Phe Cys
65 70 75 80

Trp Ala Gln Tyr Asp Pro His Thr Gln Tyr Gly Arg Thr Ala Ile Val

85

90

95

His Leu Phe Glu Trp Arg Trp Val Asp Ile Ala Lys Glu Cys Glu Arg
 100 105 110

Tyr Leu Ala Pro Asn Gly Phe Ala Gly Val Gln Val Ser Pro Pro Asn
 115 120 125

Glu Asn Ile Val Val His Ser Pro Ser Arg Pro Trp Trp Glu Arg Tyr
 130 135 140

Gln Pro Ile Ser Tyr Lys Ile Cys Ser Arg Ser Gly Asn Glu Asp Glu
 145 150 155 160

Phe Arg Asp Met Val Asn Arg Cys Asn Asn Val Gly Val Arg Ile Tyr
 165 170 175

Val Asp Ala Val Ile Asn His Met Cys Gly Val Gly Ala Gln Ala Gly
 180 185 190

Gln Ser Ser Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser
 195 200 205

<210> 213

<211> 370

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (337)

<223> N = A, C, G, OR T/U

<400> 213

gaattcgcg cgcgctcgac gtaaaaggcc taggagattt gttgatccaa taaatatgat 60
 tagggaaaca attattaggg ttcattgttcg tccttttggg gtgtggatta gcattatttg 120
 tttgataata agtttaacta gctggttgga ggttttgagg tcggccgaga agacggcact 180
 gctgcaggat gggaagagga tgggtgacta tttgttccca gacgggaagg aaatggcaga 240
 agaatatgac gagaagacca gtgaactcct tgtgaggaag tggcgtgtga aaaatgccct 300
 gggagccttg ggccagtggc agcttgaagt gggagancca gtgccctcag gagctgggag 360
 cctgggatcc 370

<210> 214

<211> 123

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (112)

<223> XAA = ANYTHING

<400> 214

Asn Ser Arg Pro Arg Arg Arg Lys Arg Pro Arg Arg Phe Val Asp Pro
 1 5 10 15
 Ile Asn Met Ile Arg Glu Thr Ile Ile Arg Val His Val Arg Pro Phe
 20 25 30
 Gly Val Trp Ile Ser Ile Ile Cys Leu Ile Ile Ser Leu Thr Ser Trp
 35 40 45
 Leu Glu Val Leu Arg Ser Ala Glu Lys Thr Ala Leu Leu Gln Asp Gly
 50 55 60
 Lys Arg Met Val His Tyr Leu Phe Pro Asp Gly Lys Glu Met Ala Glu
 65 70 75 80
 Glu Tyr Asp Glu Lys Thr Ser Glu Leu Leu Val Arg Lys Trp Arg Val
 85 90 95
 Lys Asn Ala Leu Gly Ala Leu Gly Gln Trp Gln Leu Glu Val Gly Xaa
 100 105 110
 Pro Val Pro Ser Gly Ala Gly Ser Leu Gly Ser
 115 120

<210> 215
 <211> 508
 <212> DNA
 <213> Mus musculus

<400> 215
 gaattcgcg cgcgctcgac gagatcgaga aattcgataa gtcgaagttg aagaaaacag 60
 aaacgcaaga gaaaaatcct ctgccttcaa aagaaacaat tgaacaagag aagcaagctg 120
 gcgaatcgta atgaggcgag cgccgccaat atgcaactgta cattccacga gcattgcctt 180
 cttattttac ttcttttagc tgtttaactt tgtaagatgc aaagagggtg gatcaagttt 240
 aaatgactgt gctgcccctt tcacatcaaa gaatcagaac tactgagcag gaaggcctcc 300
 cctgcctctc ccacccatct gatggtcttg ctgacagaga gggaaaagaa cttgcatggt 360
 ggtgaaggaa aaagctgggt gggagatgat gaaatagaga ggaaaattca agatgggtcaa 420
 agatgtcctg caggatgtaa aatgcagttt aatcagagtg ccattttttt ttgttcaaac 480
 aattttaatt attggaatgc acggatcc 508

<210> 216
 <211> 162
 <212> PRT
 <213> Mus musculus

<400> 216
 Asn Ser Arg Pro Arg Arg Arg Asp Arg Glu Ile Arg Val Glu Val Glu
 1 5 10 15
 Glu Asn Arg Asn Ala Arg Glu Lys Ser Ser Ala Phe Lys Arg Asn Asn
 20 25 30
 Thr Arg Glu Ala Ser Trp Arg Ile Val Met Arg Arg Ala Pro Pro Ile

35 40 45
 Cys Thr Val His Ser Thr Ser Ile Ala Phe Leu Phe Tyr Phe Phe Leu
 50 55 60
 Phe Asn Phe Val Arg Cys Lys Glu Val Gly Ser Ser Leu Asn Asp Cys
 65 70 75 80
 Ala Ala Pro Phe Thr Ser Lys Asn Gln Asn Tyr Ala Gly Arg Pro Pro
 85 90 95
 Leu Pro Leu Pro Pro Ile Trp Ser Gly Gln Arg Gly Lys Arg Thr Cys
 100 105 110
 Met Leu Val Lys Glu Lys Ala Gly Trp Glu Met Met Lys Arg Gly Lys
 115 120 125
 Phe Lys Met Val Lys Asp Val Leu Gln Asp Val Lys Cys Ser Leu Ile
 130 135 140
 Arg Val Pro Phe Phe Phe Val Gln Thr Ile Leu Ile Ile Gly Met His
 145 150 155 160
 Gly Ser

<210> 217
 <211> 920
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> (2)..(302)
 <223> N = A, C, G OR T/U

<400> 217
 tntngaattc cccagttaan agaatttggc ccaataggnc cccgggaccg gtntnggngg 60
 antcgatgtt gccaaaccag gntcncaang ttttgtaacc cngaagatga ggaggactac 120
 tnnttttcgg aagccttaag gcatnaacgt cagacagnaa naaagtgtcc aagtgggact 180
 gccgntcttc taccaatccc agccgaagaa tgctcctgtg accttcattg tgnatgganc 240
 agtagtgaaa ttgcccgaag gcttgggaaa nccaatatat atactcagaa ccaagagcct 300
 cntaagaagg tatgatgacc aaaaggacta aagacatggg caagttcagc tctgttactg 360
 tgtctaccca ttgatgaaga agaagaggag atagaggcta ggggaagttgc tgactcttac 420
 gcgcagaatg ccaaagtgat tgaaaagcag ctggagcgca aaggcatgag caagaggagg 480
 ctgcaggagt tggctgaatt ggaagccaag aaagcaaaaa tgaaggggac cctgatcgac 540
 aatcagttca aataatcaag atctttctgg gttcagactg gaggcagcag ttagatgagg 600
 aagagtagct tcaagatgtg ttttcgtttc tgtttctccc agaagggttt tctgaccatc 660
 ctattggttt tctgacactt tttcttttct tccattgaag tccttgactc catttcactt 720
 gctttctagg aggtagattg tttgtaaaat ctctgtatat atgttttctg tctttcttgt 780
 ctttgagatc aggtcttggt acataccaga gtatggcctt gaactttgtg agcctcctct 840
 cctgtcttag tctctctctc tctctctctc tctctctctc tctctctctg ctgaagttcc 900
 aggaccacac caccgatcc 920

<210> 218
 <211> 291
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (1)..(85)
 <223> XAA = ANYTHING

<400> 218

Xaa	Asn	Ser	Pro	Val	Xaa	Arg	Ile	Trp	Pro	Asn	Arg	Xaa	Pro	Gly	Pro
1				5					10					15	
Val	Xaa	Xaa	Xaa	Ser	Met	Leu	Pro	Asn	Gln	Xaa	Xaa	Xaa	Val	Leu	Pro
			20					25					30		
Xaa	Arg	Gly	Gly	Leu	Leu	Xaa	Phe	Gly	Ser	Leu	Lys	Ala	Xaa	Thr	Ser
			35				40					45			
Asp	Xaa	Xaa	Lys	Val	Ser	Lys	Trp	Asp	Cys	Arg	Ser	Ser	Thr	Asn	Pro
	50					55					60				
Ser	Arg	Arg	Met	Leu	Leu	Pro	Ser	Leu	Xaa	Met	Xaa	Gln	Asn	Leu	Pro
	65				70					75					80
Lys	Ala	Trp	Glu	Xaa	Gln	Tyr	Ile	Tyr	Ser	Glu	Pro	Arg	Ala	Ser	Glu
				85					90					95	
Gly	Met	Met	Thr	Lys	Arg	Thr	Lys	Asp	Met	Gly	Lys	Phe	Ser	Ser	Val
			100					105					110		
Thr	Val	Ser	Thr	His	Arg	Arg	Arg	Gly	Asp	Arg	Gly	Gly	Ser	Cys	Leu
			115				120					125			
Leu	Arg	Ala	Glu	Cys	Gln	Ser	Asp	Lys	Ala	Ala	Gly	Ala	Gln	Arg	His
	130					135					140				
Glu	Gln	Glu	Glu	Ala	Ala	Gly	Val	Gly	Ile	Gly	Ser	Gln	Glu	Ser	Lys
	145				150					155					160
Asn	Glu	Gly	Asp	Pro	Asp	Arg	Gln	Ser	Val	Gln	Ile	Ile	Lys	Ile	Phe
			165					170					175		
Leu	Gly	Ser	Asp	Trp	Arg	Gln	Gln	Leu	Asp	Glu	Glu	Glu	Leu	Gln	Asp
			180					185					190		
Val	Phe	Ser	Phe	Leu	Phe	Leu	Pro	Glu	Gly	Phe	Ser	Asp	His	Pro	Ile
			195				200					205			
Gly	Phe	Leu	Thr	Leu	Phe	Leu	Phe	Phe	His	Ser	Pro	Leu	His	Phe	Thr
	210					215					220				
Cys	Phe	Leu	Gly	Gly	Arg	Leu	Phe	Val	Lys	Ser	Leu	Tyr	Ile	Cys	Phe

Glu Ser Val Trp Gly Ala Lys Val Arg Ser Arg Tyr Asp Ser His Pro
 50 55 60
 Asn Cys Leu Glu Ser Ala Tyr Met Thr Val Phe Phe Ser Ile Leu Phe
 65 70 75 80
 Phe Leu Ser Ser Ser Thr His Thr Leu Ala Ser Phe Gly Gly Lys Leu
 85 90 95
 Asn Lys Arg Thr Glu Phe Pro Ser Pro Arg Val Thr Tyr Glu Met Thr
 100 105 110
 Gln Leu Pro Phe Ser Leu Lys Gly Phe Leu Ser Ser Gly Ile Pro Phe
 115 120 125
 Thr Arg Gly Ser
 130

<210> 221
 <211> 244
 <212> DNA
 <213> Mus musculus
 <220>
 <221> modified_base
 <222> (210)
 <223> N = A, C, G OR T/U

<400> 221
 gaattcgcg cgcgctcgac ggagtcttct gactgctggt ggagcaggtc tcaggaatct 60
 cttcgcttca gcttcaatca tggcctgtgg tctggctgcc agcaacctga atctcaaacc 120
 tggggaatgt ctcaaagttc ggggagaggt ggcctcggac gccaaagagct ttgtgctgaa 180
 cctgggaaaa gacagcaaca acctgtgccn acacttcaat cctcgcttca atgcacatgg 240
 atcc 244

<210> 222
 <211> 81
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (70)
 <223> XAA = ANYTHING

<400> 222
 Asn Ser Arg Pro Arg Arg Arg Ser Leu Leu Thr Ala Gly Gly Ala Gly
 1 5 10 15

Leu Arg Asn Leu Phe Ala Ser Ala Ser Ile Met Ala Cys Gly Leu Val
 20 25 30

Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Lys Val Arg Gly

35

40

45

Glu Val Ala Ser Asp Ala Lys Ser Phe Val Leu Asn Leu Gly Lys Asp
 50 55 60

Ser Asn Asn Leu Cys Xaa His Phe Asn Pro Arg Phe Asn Ala His Gly
 65 70 75 80

Ser

<210> 223

<211> 142

<212> DNA

<213> Mus musculus

<400> 223

gaattcgcg cgcgctcgac gttcattatt tttggttggt tgtcttgggt tagcattaaa 60
 gccttcacct atttatggag gtttaggttt aattgttagt gggtttggtt gttgtttaat 120
 ggttttaggg tttggtggat cc 142

<210> 224

<211> 55

<212> PRT

<213> Mus musculus

<400> 224

Ile Glu Lys Gly Arg Val Ser Leu Asn Ser Arg Pro Arg Arg Arg Ser
 1 5 10 15

Leu Phe Leu Val Gly Cys Leu Gly Leu Ala Leu Lys Pro Ser Pro Ile
 20 25 30

Tyr Gly Gly Leu Gly Leu Ile Val Ser Gly Phe Val Gly Cys Leu Met
 35 40 45

Val Leu Gly Phe Gly Gly Ser
 50 55

<210> 225

<211> 394

<212> DNA

<213> Mus musculus

<400> 225

gaattcgcg cgcgctcgac tttttttttt ttttttttga tttttccaag ataaaacttt 60
 attggagaca gcaaggagta tactgaaagt gggggagcca tgccttcatt ccataactgc 120
 aatcagatgc tctcctctga gagagagtgt gtggggagcc aaggtgagaa gcaggatga 180
 ttcacacccc aactgcttg agagtgtta tatgacagtc tttttctcga ttttattttt 240
 tctcagttct tcaacacaca ctttggttc atttggggga aaattaaaca aaagaacaga 300
 atttccctcc cccagagtta cttatgaaat gacacagctg cccttttctt tgaagggatt 360
 cttgtcttct gggattccct ttaccagagg atcc 394

<210> 226
 <211> 130
 <212> PRT
 <213> Mus musculus

<400> 226
 Asn Ser Arg Pro Arg Arg Leu Phe Phe Phe Phe Phe Phe Phe Gln Asp
 1 5 10 15
 Lys Thr Leu Leu Glu Thr Ala Arg Ser Ile Leu Lys Val Gly Glu Pro
 20 25 30
 Cys Leu His Ser Ile Thr Ala Ile Arg Cys Ser Pro Leu Arg Glu Ser
 35 40 45
 Val Trp Gly Ala Lys Val Arg Ser Arg Tyr Asp Ser His Pro Asn Cys
 50 55 60
 Leu Glu Ser Ala Tyr Met Thr Val Phe Phe Ser Ile Leu Phe Phe Leu
 65 70 75 80
 Ser Ser Ser Thr His Thr Leu Ala Ser Phe Gly Gly Lys Leu Asn Lys
 85 90 95
 Arg Thr Glu Phe Pro Ser Pro Arg Val Thr Tyr Glu Met Thr Gln Leu
 100 105 110
 Pro Phe Ser Leu Lys Gly Phe Leu Ser Ser Gly Ile Pro Phe Thr Arg
 115 120 125
 Gly Ser
 130

<210> 227
 <211> 480
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (21)..(36)
 <223> N - A, C, G OR T/U

<400> 227
 gaattcgcg cgcgctcgac nttttttttt tttttntttt tttttttttt tttttttttt 60
 ttttaagaaca actgaacata tgttgtgtgt accgggcata aaggatgaat gggcccttta 120
 gttaaccacac tgcttgata acatgacact tagtccactt ccatctctcc ggagtcggtg 180
 tgctgtgagc ttcctttggg tggatctggg ctggtctctg aaccactctg tccgtccatt 240
 ggtccattgt gctcactacc agtttttgct ttgtcttcag gagcttctac ttttggtttg 300
 ggcttataaa cgatggggtt acagaaatta tccagttcct ttgactttgt aactatttct 360
 gacactttta ccacgggata ttgagtgaga ctttaattat tctgtgcatt catcttactg 420
 tttagccagt tcatggagtc actgatgtac ttttcaactc tttccatttc agcaggatcc 480

<210> 228
 <211> 154
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (12)
 <223> XAA = ANYTHING

<400> 228
 Glu Phe Ala Ala Ala Ser Thr Phe Phe Phe Phe Xaa Phe Phe Phe Phe
 1 5 10 15
 Phe Phe Phe Phe Phe Lys Asn Asn Thr Tyr Val Val Cys Thr Gly His
 20 25 30
 Lys Gly Met Gly Pro Leu Val Asn Pro Leu Leu Gly His Asp Thr Ser
 35 40 45
 Thr Ser Ile Ser Pro Glu Ser Val Cys Cys Glu Leu Pro Leu Gly Gly
 50 55 60
 Ser Gly Leu Val Ser Glu Pro Leu Cys Pro Ser Ile Gly Pro Leu Cys
 65 70 75 80
 Ser Leu Pro Val Phe Ala Leu Ser Ser Gly Ala Ser Thr Phe Gly Leu
 85 90 95
 Gly Leu Thr Met Gly Leu Gln Lys Leu Ser Ser Ser Phe Asp Phe Val
 100 105 110
 Thr Ile Ser Asp Thr Phe Thr Thr Gly Ser Val Arg Leu Asn Leu Phe
 115 120 125
 Cys Ala Phe Ile Leu Leu Phe Ser Gln Phe Met Glu Ser Leu Met Tyr
 130 135 140
 Phe Ser Thr Leu Ser Ile Ser Ala Gly Ser
 145 150

<210> 229
 <211> 420
 <212> DNA
 <213> Mus musculus

<400> 229
 gaattcgcg cgcgctcgac tttttttttt tttttttttt tttttttttt tttttttttt 60
 ttttgatttt tccaagataa aactttattg gagacagcaa ggagtataact gaaagtgggg 120
 gagccatgcc ttcattccat aactgcaatc agatgctctc ctctgagaga gagtgtgtgg 180
 ggagccaagg tgagaagcag gtatgattca caccccaact gcttggagag tgcttatatg 240
 acagtctttt tctcgatttt attttttctc agttcttcaa cacacacttt ggcttcattt 300

gggggaaaat taaacaaaag aacagaattt cctccccca gagttactta tgaaatgaca 360
cagctgccct tttctttgaa gggattcttg tcttctggga ttccctttac cagaggatcc 420

<210> 230
<211> 139
<212> PRT
<213> Mus musculus

<400> 230
Glu Phe Ala Ala Ala Ser Thr Phe Phe Phe Phe Phe Phe Phe Phe
1 5 10 15
Phe Phe Phe Phe Phe Phe Phe Gln Asp Lys Thr Leu Leu Glu Thr Ala
20 25 30
Arg Ser Ile Leu Lys Val Gly Glu Pro Cys Leu His Ser Ile Thr Ala
35 40 45
Ile Arg Cys Ser Pro Leu Arg Glu Ser Val Trp Gly Ala Lys Val Arg
50 55 60
Ser Arg Tyr Asp Ser His Pro Asn Cys Leu Glu Ser Ala Tyr Met Thr
65 70 75 80
Val Phe Phe Ser Ile Leu Phe Phe Leu Ser Ser Ser Thr His Thr Leu
85 90 95
Ala Ser Phe Gly Gly Lys Leu Asn Lys Arg Thr Glu Phe Pro Ser Pro
100 105 110
Arg Val Thr Tyr Glu Met Thr Gln Leu Pro Phe Ser Leu Lys Gly Phe
115 120 125
Leu Ser Ser Gly Ile Pro Phe Thr Arg Gly Ser
130 135

<210> 231
<211> 629
<212> DNA
<213> Mus musculus

<400> 231
gaattcgcg cgcgctcgac gtcactgtgg agctcagatc acagtgtctga cagaatccat 60
atttgagaaa ttacataagg tttgaaagag aggatagtga aaggatacga attcctaaaa 120
acgtttaatc tggccttttg tttgaacgaa agagaaaattg aaaccaaattg aaataaatta 180
cttggttagaa agaatactgc caacagcata gcaaaaatgaa attcttctctg ctgctttccc 240
tcattggatt ctgctgggcc caatatgacc cacatactca atatggacga actgctattg 300
tccacctgtt tgagtggcgc tgggttgata ttgctaagga atgtgagaga tacttagctc 360
ctaattgatt tgcaggtgtg caggtctctc cacccaatga aaacatcgta gtccacagcc 420
cttcaagacc atggtgggaa agatatcaac caattagcta caaaatatgt tccaggtctg 480
gaaatgaaga tgaattcagg gacatggtga acaggtgcaa caatgttggt gtccgtattt 540
atgtggatgc tgtcattaac cacatgtgtg gagtgggggc tcaagctgga caaagcagta 600
catgtggaag ttatttcaac cccggatcc 629

<210> 232
 <211> 204
 <212> PRT
 <213> Mus musculus

<400> 232
 Ile Arg Gly Arg Val Asp Val Thr Val Glu Leu Arg Ser Gln Cys Gln
 1 5 10 15
 Asn Pro Tyr Leu Glu Asn Tyr Ile Arg Phe Glu Arg Glu Asp Ser Glu
 20 25 30
 Arg Ile Arg Ile Pro Lys Asn Val Ser Gly Leu Leu Phe Glu Arg Lys
 35 40 45
 Arg Asn Asn Gln Met Lys Ile Thr Cys Lys Glu Tyr Cys Gln Gln His
 50 55 60
 Ser Lys Met Lys Phe Phe Leu Leu Leu Ser Leu Ile Gly Phe Cys Trp
 65 70 75 80
 Ala Gln Tyr Asp Pro His Thr Gln Tyr Gly Arg Thr Ala Ile Val His
 85 90 95
 Leu Phe Glu Trp Arg Trp Val Asp Ile Ala Lys Glu Cys Glu Arg Tyr
 100 105 110
 Leu Ala Pro Asn Gly Phe Ala Gly Val Gln Val Ser Pro Pro Asn Glu
 115 120 125
 Asn Ile Val Val His Ser Pro Ser Arg Pro Trp Trp Glu Arg Tyr Gln
 130 135 140
 Pro Ile Ser Tyr Lys Ile Cys Ser Arg Ser Gly Asn Glu Asp Glu Phe
 145 150 155 160
 Arg Asp Met Val Asn Arg Cys Asn Asn Val Gly Val Arg Ile Tyr Val
 165 170 175
 Asp Ala Val Ile Asn His Met Cys Gly Val Gly Ala Gln Ala Gly Gln
 180 185 190
 Ser Ser Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser
 195 200

<210> 233
 <211> 254
 <212> DNA
 <213> Mus musculus

<400> 233
 gaattcgagg ccgcgtcgac ggatttttct tgagaaaatc ttgggtgaga ttattctgga 60

ttctatttaa atgtgtgtat ataatgatta ggattttatt ttacagtca tatctacttc 120
 cttccttatg tgcgaaatct attgcaacat attatgcacc atactcaaat ccctgggtgtt 180
 ccagccaagg ttcttgggtt tcaccacagt acagtaatgt gactccaata ccagaaggaa 240
 agaatgtggg atcc 254

<210> 234
 <211> 84
 <212> PRT
 <213> Mus musculus

<400> 234
 Ile Arg Gly Arg Val Asp Gly Phe Phe Leu Arg Lys Ser Trp Val Arg
 1 5 10 15
 Leu Phe Trp Ile Leu Phe Lys Cys Val Tyr Ile Met Ile Arg Ile Leu
 20 25 30
 Phe Leu Gln Ser Tyr Leu Leu Pro Ser Leu Cys Ala Lys Ser Ile Ala
 35 40 45
 Thr Tyr Tyr Ala Pro Tyr Ser Asn Pro Trp Cys Ser Ser Gln Gly Ser
 50 55 60
 Trp Val Ser Pro Gln Tyr Ser Asn Val Thr Pro Ile Pro Glu Gly Lys
 65 70 75 80
 Asn Val Gly Ser

<210> 235
 <211> 660
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (10)..(166)
 <223> N = A, C, G OR T/U

<400> 235
 gtcacccaan actgcggcat tatgaggaca ttatgacgaa ataagggttaa aaaagaagtg 60
 aagaacagtt ggggtccagt gcaaganac acggccaggn tggcaaaaana gtgcagcggc 120
 acaggccgat tggaaaccgac atgaggatct acgcaaccga ctcggncagt accgcaacga 180
 ggtgcacacc atgctgggccc agagcacaga gaagatacgg gcgcggctct ccacacacct 240
 gcgcaagatg cgcaagcgct tgatgcggga tgccgaggat ctgcagaagc gcctagctgt 300
 gtacaagcag gggcacgcga gggcgccgag cgcggtgtga gtgccatccg tgagcgcttg 360
 gggcctctgg tggagcaagg tcgccagcgc accgccaacc taggcgctgg ggccgcccag 420
 cctctgcgcg atcgcgccca ggcttttggg gaccgcatcc gagggcggtt ggaggaagtg 480
 ggcaaccagg cccgtgaccg cctagaggag gtgcgtgagc acatggagga ggtgcgctcc 540
 aagatggagg aactctcgag tcccagcatc agagcgctg gaccttttcc cgcgctccgc 600
 agcatgcagg tctcccgtgt gctggccgcg ctgtgcggca tgctactctg cgccggatcc 660

<210> 236
 <211> 218
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (4) .. (54)
 <223> XAA = ANYTHING

<400> 236
 Val Thr Gln Xaa Cys Gly Ile Met Arg Thr Leu Arg Asn Lys Val Lys
 1 5 10 15
 Lys Glu Val Lys Asn Ser Trp Val Gln Trp Arg Arg Xaa Thr Ala Arg
 20 25 30
 Xaa Ala Lys Xaa Cys Ser Gly Thr Gly Arg Leu Glu Pro Thr Gly Ser
 35 40 45
 Thr Gln Pro Thr Arg Xaa Val Pro Gln Arg Gly Ala His His Ala Gly
 50 55 60
 Pro Glu His Arg Glu Asp Thr Gly Ala Ala Leu His Thr Pro Ala Gln
 65 70 75 80
 Asp Ala Gln Ala Leu Asp Ala Gly Cys Arg Gly Ser Ala Glu Ala Pro
 85 90 95
 Ser Cys Val Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Val Ser
 100 105 110
 Ala Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Gln Arg
 115 120 125
 Thr Ala Asn Leu Gly Ala Gly Ala Ala Gln Pro Leu Arg Asp Arg Ala
 130 135 140
 Gln Ala Phe Gly Asp Arg Ile Arg Gly Arg Leu Glu Glu Val Gly Asn
 145 150 155 160
 Gln Ala Arg Asp Arg Leu Glu Glu Val Arg Glu His Met Glu Glu Val
 165 170 175
 Arg Ser Lys Met Glu Glu Leu Ser Ser Pro Ser Ile Arg Ala Arg Gly
 180 185 190
 Pro Phe Pro Ala Ser Arg Ser Met Gln Val Ser Arg Val Leu Ala Ala
 195 200 205
 Leu Cys Gly Met Leu Leu Cys Ala Gly Ser
 210 215

<210> 237

<211> 519
 <212> DNA
 <213> Mus musculus

<400> 237
 cctgcaggag atatatccag agctgcagat cacaaatgtg atgaagcaaa ccagccagtc 60
 aatattgata gttggtgccg aagggacaaa aggcagtgc agagtcacat tggtatacca 120
 ttcaagtgtc ttgtgggtga atttgtaagt gatgtcctgc tagttccaga taactgccag 180
 tttttccacc aagagcggat ggaggtgtgt gagaagcacc agcgctggca cacgttagtc 240
 aaggaggcat gtctgactga ggggctgacc ttatatagct atggcatgct gctgccctgc 300
 ggggtagacc agttccatgg caccgagtat gtgtgctgcc ctcagacaaa gactgttgac 360
 tcggactcga ctatgtccaa agaagaggag gaagaggaag aggatgaaga ggacgaagag 420
 gaagactatg atcttgataa aagtgaattt cctactgaag cagatttgga agacttcaca 480
 gaagcagcag cagatgagga agaagaggat gagggatcc 519

<210> 238
 <211> 173
 <212> PRT
 <213> Mus musculus

<400> 238
 Pro Ala Gly Asp Ile Ser Arg Ala Ala Asp His Lys Cys Asp Glu Ala
 1 5 10 15
 Asn Gln Pro Val Asn Ile Asp Ser Trp Cys Arg Arg Asp Lys Arg Gln
 20 25 30
 Cys Lys Ser His Ile Val Ile Pro Phe Lys Cys Leu Val Gly Glu Phe
 35 40 45
 Val Ser Asp Val Leu Leu Val Pro Asp Asn Cys Gln Phe Phe His Gln
 50 55 60
 Glu Arg Met Glu Val Cys Glu Lys His Gln Arg Trp His Thr Leu Val
 65 70 75 80
 Lys Glu Ala Cys Leu Thr Glu Gly Leu Thr Leu Tyr Ser Tyr Gly Met
 85 90 95
 Leu Leu Pro Cys Gly Val Asp Gln Phe His Gly Thr Glu Tyr Val Cys
 100 105 110
 Cys Pro Gln Thr Lys Thr Val Asp Ser Asp Ser Thr Met Ser Lys Glu
 115 120 125
 Glu Glu Glu Glu Glu Glu Asp Glu Glu Asp Glu Glu Glu Asp Tyr Asp
 130 135 140
 Leu Asp Lys Ser Glu Phe Pro Thr Glu Ala Asp Leu Glu Asp Phe Thr
 145 150 155 160
 Glu Ala Ala Ala Asp Glu Glu Glu Glu Asp Glu Gly Ser
 165 170

<210> 239
 <211> 678
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (9)..(160)
 <223> N = A, C, G OR T/U

<400> 239
 gtggcccant ccggcccntg cccagtgngt ggctccngct ggcacgccag cggccttgga 60
 agaagctcaa gcccatgagg ccggcgcgcc ntgccgccgg tgcaaaagag acggagctcc 120
 cggccccgc ggggtggagcg ggggatcaat gcggttcagn aatcgattcc agcgtttcat 180
 gaaccatcgg gccccagtaa tggccgctac aaaccaacgt gctacgaaca tgctgccaat 240
 tgctacacac acgcattcct cattgttccg gccattgtgg gcagtgccct cctccatcgg 300
 ctgtctgatg actgctggga gaagataaca gcatggatct acgggatggg cttttgtgcc 360
 ctcttcacag tctccacagt gtttcacata gtatcatgga agaagagcca cttgagaaca 420
 gtggagcatt gtttccacat gtgcgatcgg atggatcatct acttcttcat tgctgcttcc 480
 tacgccccat gggttaaactt ccgtgaactt ggacccttgg catctcatat gcgttggttt 540
 atctggetca tggcagctgg aggaaccatt tatgtatttc tctaccatga aaagtataaa 600
 gtggttgaaac ttttcttcta tctcacgatg ggattttctc cagccttggt ggtgacatca 660
 atgaataaca ctggatcc 678

<210> 240
 <211> 225
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (3)..(53)
 <223> XAA = ANYTHING

<400> 240
 Val Ala Xaa Ser Gly Pro Cys Pro Val Xaa Gly Ser Xaa Trp His Ala
 1 5 10 15
 Ser Gly Leu Gly Arg Ser Ser Ser Pro Gly Arg Arg Ala Xaa Pro Pro
 20 25 30
 Val Gln Lys Arg Arg Ser Ser Arg Pro Pro Arg Val Glu Arg Gly Ile
 35 40 45
 Asn Ala Val Gln Xaa Ser Ile Pro Ala Phe His Glu Pro Ser Gly Pro
 50 55 60
 Ser Asn Gly Arg Tyr Lys Pro Thr Cys Tyr Glu His Ala Ala Asn Cys
 65 70 75 80
 Tyr Thr His Ala Phe Leu Ile Val Pro Ala Ile Val Gly Ser Ala Leu
 85 90 95

Leu His Arg Leu Ser Asp Asp Cys Trp Glu Lys Ile Thr Ala Trp Ile
 100 105 110

Tyr Gly Met Gly Leu Cys Ala Leu Phe Ile Val Ser Thr Val Phe His
 115 120 125

Ile Val Ser Trp Lys Lys Ser His Leu Arg Thr Val Glu His Cys Phe
 130 135 140

His Met Cys Asp Arg Met Val Ile Tyr Phe Phe Ile Ala Ala Ser Tyr
 145 150 155 160

Ala Pro Trp Leu Asn Leu Arg Glu Leu Gly Pro Leu Ala Ser His Met
 165 170 175

Arg Trp Phe Ile Trp Leu Met Ala Ala Gly Gly Thr Ile Tyr Val Phe
 180 185 190

Leu Tyr His Glu Lys Tyr Lys Val Val Glu Leu Phe Phe Tyr Leu Thr
 195 200 205

Met Gly Phe Ser Pro Ala Leu Val Val Thr Ser Met Asn Asn Thr Gly
 210 215 220

Ser
 225

<210> 241
 <211> 655
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (16)..(85)
 <223> N = A, C, G OR T/U

<400> 241
 gttgtagatc tgaaancaa aaagaaggcg gggcttgagg tcttgaggtc acttaagggc 60
 caccntnttt gacntaagac ctcantaggc cccgcctcta aagggttctg acctcaatag 120
 gccttctctgg agaactagtt tctaactctc aggcccttgg gacattgcat ctcagtagta 180
 ggtgcctctc tacctgtggt tggcttggtc atgattggca gacactctgc ctggctctgc 240
 acagcagcgg ctcagcatca gcatccagct gcttgctgtg tgtagttgt ctcacagctg 300
 agggctctgc ctcggctact tcaggcttcc cggttaggaa gataatttgg tcaattgtgt 360
 ctgtggccac tcttagaatt ttctcttttg agggaaacctg tgactgggtg gcttttgcac 420
 tctatggagg gagatggggg taaagactgt ggcaacacac accctccaga agagctggga 480
 ccagagactg tcagcacaga aaggacaatg tcttttttag tagctgtggc agacttgagt 540
 tgctgtaatt tatacaaatt gtttagaatg gtttttaaga ctaagaaggg aaatatactt 600
 attgcacaag acttttataa ttactatact taaattatgc tctatgtggg gatcc 655

<210> 242
 <211> 201
 <212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (3)..(25)

<223> XAA = ANYTHING

<400> 242

Leu Ile Xaa Gln Glu Arg Arg Arg Gly Leu Arg Ser Gly His Leu Arg
1 5 10 15

Ala Thr Xaa Phe Asp Xaa Arg Pro Xaa Ala Pro Pro Leu Lys Val Ser
20 25 30

Asp Leu Asn Arg Pro Ser Trp Arg Thr Ser Phe Leu Ser Gly Pro Trp
35 40 45

Asp Ile Ala Ser Gln Val Pro Leu Tyr Leu Cys Leu Ala Cys Ser Leu
50 55 60

Ala Asp Thr Leu Pro Gly Ser Ala Gln Gln Arg Leu Ser Ile Ser Ile
65 70 75 80

Gln Leu Leu Ala Val Cys Leu Ser His Ser Gly Leu Cys Leu Gly Tyr
85 90 95

Phe Arg Leu Ser Gly Glu Asp Asn Leu Val Thr Cys Val Cys Gly His
100 105 110

Ser Asn Phe Leu Phe Gly Asn Leu Leu Val Gly Phe Cys Ile Leu Trp
115 120 125

Arg Glu Met Gly Leu Lys Thr Val Ala Thr His Thr Leu Gln Lys Ser
130 135 140

Trp Asp Gln Arg Leu Ser Ala Gln Lys Gly Gln Cys Leu Phe Leu Trp
145 150 155 160

Gln Thr Val Ala Val Ile Tyr Thr Asn Cys Leu Glu Trp Phe Leu Arg
165 170 175

Leu Arg Arg Glu Ile Tyr Leu Leu His Lys Thr Phe Ile Ile Thr Ile
180 185 190

Leu Lys Leu Cys Ser Met Trp Gly Ser
195 200

<210> 243

<211> 677

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (1)

<223> N = A, C, G OR T/U

<400> 243

```
ncgctgtagt ttcatttctc actttgaggg cacagatgaa aatgtatatc gcaacacagt 60
ggatatcagc ccaagcacga agaccatgct gaacatgcac ccgtacagag tgtacttaaa 120
ggagtcgtca taagggcact gggagccatt ggagcttacc attgtcaggc agtgcagctt 180
acaggaggcc ttttgtccgc agcgcttgat cgatcgccctt tgctattcag atgtgggtcac 240
agcagcagcc agtttatttg caaagtattt gtttcttttc ctgttcttac aaatactttc 300
ttctcttaac tcttcaaagg aaacatgaaa tgtgttccgt aaaagtttct agtagattat 360
tcaggaaaat agtctgattt tctggctcag aaaatccatg agtctggagt ttagttaact 420
gacagaaaat gcagtcaagg aagccaaccc ataaagctga aagtgttaagg aaaaactgtt 480
ccaagtcgga ccagaccagt ccgcgtggaa acttgtgctt cagccgccag ggtccaaacc 540
agctttactt cagtcacaaa cactcgccgt gcgtccgtcc gcccgctcgtc ctcggttact 600
tcttccttct ttttattctc aaactttgta tttctacatt gattccggac ggcgataggc 660
agtcgtttaa gggatcc 677
```

<210> 244

<211> 219

<212> PRT

<213> Mus musculus

<400> 244

```
Ala Val Val Ser Phe Leu Thr Leu Arg Ala Gln Met Lys Met Tyr Ile
  1              5              10              15
```

```
Ala Thr Gln Trp Ile Ser Ala Gln Ala Arg Arg Pro Cys Thr Cys Thr
      20              25              30
```

```
Arg Thr Glu Cys Thr Arg Ser Arg His Lys Gly Thr Gly Ser His Trp
      35              40              45
```

```
Ser Leu Pro Leu Ser Gly Ser Ala Ala Tyr Arg Arg Pro Phe Val Arg
      50              55              60
```

```
Ser Ala Ser Ile Ala Phe Ala Ile Gln Met Trp Ser Gln Gln Gln Pro
      65              70              75              80
```

```
Val Tyr Leu Gln Ser Ile Cys Phe Phe Ser Cys Ser Tyr Lys Tyr Phe
      85              90              95
```

```
Leu Leu Leu Thr Leu Gln Arg Lys His Glu Met Cys Ser Val Lys Val
      100             105             110
```

```
Ser Ser Arg Leu Phe Arg Lys Ile Val Phe Ser Gly Arg Glu Asn Pro
      115             120             125
```

```
Val Trp Ser Leu Val Asn Gln Lys Met Gln Ser Arg Lys Pro Thr His
      130             135             140
```

```
Lys Ala Glu Ser Val Arg Lys Asn Cys Ser Lys Ser Asp Gln Thr Ser
      145             150             155             160
```

```
Pro Arg Gly Asn Leu Cys Phe Ser Arg Gln Gly Pro Asn Gln Leu Tyr
```

165

170

175

Phe Ser His Lys His Ser Pro Cys Val Arg Pro Pro Val Val Leu Gly
 180 185 190

Tyr Phe Phe Leu Leu Phe Ile Leu Lys Leu Cys Ile Ser Thr Leu Ile
 195 200 205

Pro Asp Gly Asp Arg Gln Ser Phe Lys Gly Ser
 210 215

<210> 245

<211> 660

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (7)..(45)

<223> N = A, C, G OR T/U

<400> 245

agagatncaa tctaaaaagc agatantgag cagagactan ggagnagtta acatactaaa 60
 ccgctacata cataggacaa atgccatttg gaggtgaag tcaaggaaac atcagtatac 120
 atgtaagttt ggcattgtat ttggttgca ttaaattgaa agggcttttg tactgagttg 180
 agatcttatt tcctagataa tagagtgtat tgggtttgaa taggaagtgt catggacaga 240
 gctctgagcc tgtaggagca aggagtatca caaaggctct ttgccacagc ccaggcaagc 300
 aatctagagc ttaagcctag ggtggcagat gtgtggaaga acacagacac agttgtgcag 360
 agcctgggaa acggcttggtg cttccaggga agaggtttat gttatcgttg tttgggttg 420
 gttgtttatt tctgggggct gggggaggga aggtatgtat gttttgttg ttagtatctc 480
 atgtagccag gatggccttg aactcactat gtagctcaga ctgacgtgga attccaggtt 540
 ctctctttac tccccacact ggtagctgtg caccataaaa cctggcttat actttgtaaa 600
 atcccaatat tctcttgctt gctttcagca cccttatcac atgtgtggat tctgggatcc 660

<210> 246

<211> 211

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (3)..(14)

<223> XAA = ANYTHING

<400> 246

Arg Asp Xaa Ile Lys Ala Asp Xaa Glu Gln Arg Leu Xaa Xaa Ser His
 1 5 10 15

Thr Lys Pro Leu His Thr Asp Lys Cys His Leu Glu Ala Glu Val Lys
 20 25 30

Glu Thr Ser Val Tyr Met Val Trp His Cys Ile Trp Leu Arg Leu Asn
 35 40 45

Gly Lys Gly Phe Cys Thr Glu Leu Arg Ser Tyr Leu Leu Asp Asn Arg
 50 55 60

Val Tyr Trp Val Ile Gly Ser Val Met Asp Arg Ala Leu Ser Leu Glu
 65 70 75 80

Gln Gly Val Ser Gln Arg Leu Phe Ala Thr Ala Gln Ala Ser Asn Leu
 85 90 95

Glu Leu Lys Pro Arg Val Ala Asp Val Trp Lys Asn Thr Asp Thr Val
 100 105 110

Val Gln Ser Leu Gly Asn Gly Leu Gly Phe Gln Gly Arg Gly Leu Cys
 115 120 125

Tyr Arg Cys Leu Gly Trp Val Val Tyr Phe Trp Gly Leu Gly Glu Gly
 130 135 140

Arg Tyr Val Cys Phe Val Val Tyr Leu Met Pro Gly Trp Pro Thr His
 145 150 155 160

Tyr Val Ala Gln Thr Asp Val Glu Phe Gln Val Leu Ser Leu Leu Pro
 165 170 175

Thr Leu Val Ala Val His His Lys Thr Trp Leu Ile Leu Cys Lys Ile
 180 185 190

Pro Ile Phe Ser Cys Leu Leu Ser Ala Pro Leu Ser His Val Trp Ile
 195 200 205

Leu Gly Ser
 210

<210> 247

<211> 673

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (4)..(173)

<223> N = A, C, G, OR T/U

<400> 247

gttnnnnncc nttnnnnna anttnttnnn aatnaaaaag nanantaann nmanntnnnn 60
 ncngnttnnn ccccnnttcc nnnnnnctan gnnncnggct tnannttggg gttantngnn 120
 ntggtaatac nngggggccaa gcntgcntgt gtaaagcaag nccctnantg agnttctcct 180
 catcagcggg gttcagacct ggctggtttg taggtacact agccacgatc agcacaagtc 240
 acaagtgcc ctcacttaca cccatcccc cagcctaaaa ctttctccta aggtgccaa 300
 ggatcagtc gtctgaagga tgaaaaccag agcgtggtgt acagctctcc ctttcaaact 360
 gaagccaccc tgggggacgg gggtatcgtt atcccacgtt taaccataaa tagggctcctg 420
 atgaaaagg ggaaggaaaa aaagactact ctaacagcaa atttttcttt tttagggtta 480
 aaactcttgc taaaattcct agtgaatcag tgctttggaa taaaagtatc ataagccaat 540

gccacaggta tcatacgcta atgtcagggg ggtgctatgg gtgtcctttt gttgctgttt 600
 tgttctgttt tctttcctat gtcaatgtgg cttcacaagt gtgggatttc aagaggtgaa 660
 gatacatgga tcc 673

<210> 248
 <211> 210
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (1)..(56)
 <223> XAA = ANYTHING

<400> 248

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Lys	Xaa	Xaa	Xaa
1				5					10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20				25						30		
Ala	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Trp	Tyr	Xaa	Gly	Pro	Ser	Xaa	Xaa
		35					40					45			
Val	Ser	Lys	Xaa	Leu	Xaa	Glu	Xaa	Leu	Leu	Ile	Ser	Gly	Val	Gln	Thr
	50					55					60				
Trp	Leu	Val	Cys	Arg	Tyr	Thr	Ser	His	Asp	Gln	His	Lys	Ser	Gln	Val
65					70					75					80
Pro	Leu	Thr	Tyr	Thr	His	Pro	Pro	Ser	Leu	Lys	Leu	Ser	Pro	Lys	Val
					85					90				95	
Pro	Arg	Asp	Gln	Ser	Val	Arg	Met	Lys	Thr	Arg	Ala	Trp	Cys	Thr	Ala
			100					105					110		
Leu	Pro	Phe	Lys	Leu	Lys	Pro	Pro	Trp	Gly	Thr	Gly	Val	Ser	Leu	Ser
	115						120					125			
His	Val	Pro	Ile	Gly	Ser	Lys	Gly	Gly	Arg	Lys	Lys	Arg	Leu	Leu	Gln
	130					135					140				
Gln	Ile	Phe	Leu	Phe	Val	Asn	Ser	Cys	Asn	Ser	Ile	Ser	Ala	Leu	Glu
145					150				155					160	
Lys	Tyr	His	Lys	Pro	Met	Pro	Gln	Val	Ser	Tyr	Ala	Asn	Val	Arg	Glu
				165					170				175		
Val	Leu	Trp	Val	Ser	Phe	Cys	Cys	Cys	Phe	Val	Leu	Phe	Ser	Phe	Leu
			180					185					190		
Cys	Gln	Cys	Gly	Phe	Thr	Ser	Val	Gly	Phe	Gln	Glu	Val	Lys	Ile	His
			195				200					205			

Gly Ser
210

<210> 249
<211> 656
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (2)..(68)
<223> N = A, C, G OR T/U

<400> 249
anaattcgcg ncggcgctcga cgctaacca aaaacacagg tcagttttgg agaccctcac 60
acagatcntg gaatgagatc tgcagccagg tgtccagccc aggcttgggc ttctcattgt 120
acccaaggct ggaaggggtt ggtctgtact aacacacaag ctgcagtc cc tgcttgactg 180
ctggcttccc aaagaggaga cattggtctt gctgggaggg acagcaggag agtgaccac 240
tgccactgca ctctaactga gtactaaggc cactagggct ttctagacct cgctttcccc 300
ttgagcttcc tggggagggt aagtggaggt tgtgtgtgtg tgtgtgtctt tgtgtgttta 360
gatttattgc agggaaaggt ctaatccaga atcagtattc aggctttgtc atgttgatc 420
agtgccaaagg tgaccctcaa ggtcatgtaa ctttaagcaa gcttagcatt tattttattc 480
ctgaaaactt aagtatttta cttttttgtg tgttcgtgga gacatttgca gtattaatga 540
ttttattttt cctaaatcgg gatggaaaca aacttttcca gggtatgta ataagccact 600
taagtgcctt aaacagcttt ggtgtagatg agaattgctg ggtccgctcat ggatcc 656

<210> 250
<211> 214
<212> PRT
<213> Mus musculus

<400> 250
Asn Ser Arg Arg Arg Arg Arg Leu Thr Lys Asn Thr Gly Gln Phe Trp
1 5 10 15
Arg Pro Ser His Arg Ser Trp Asn Glu Ile Cys Ser Gln Val Ser Ser
20 25 30
Pro Gly Leu Gly Phe Ser Leu Tyr Pro Arg Leu Glu Gly Phe Gly Leu
35 40 45
Tyr His Thr Ser Ser Gln Ser Cys Leu Thr Ala Gly Phe Pro Lys Arg
50 55 60
Arg His Trp Ser Cys Trp Glu Ala Gln Gln Glu Ser Asp Pro Leu Pro
65 70 75 80
Leu His Ser Asn Val Leu Arg Pro Leu Gly Leu Ser Arg Pro Arg Phe
85 90 95
Pro Leu Glu Leu Pro Gly Glu Val Lys Gly Val Cys Val Cys Val Cys
100 105 110

Leu Cys Val Leu Arg Phe Ile Ala Gly Lys Gly Leu Ile Gln Asn Gln
115 120 125

Tyr Ser Gly Phe Val Met Leu Tyr Gln Cys Gln Gly Asp Pro Gln Gly
130 135 140

His Val Thr Ala Lys Leu Ser Ile Tyr Phe Ile Pro Glu Asn Leu Ser
145 150 155 160

Ile Leu Leu Phe Cys Val Phe Val Glu Thr Phe Ala Val Leu Met Ile
165 170 175

Leu Phe Phe Leu Asn Arg Asp Gly Asn Lys Leu Phe Gln Val Met Leu
180 185 190

Ile Ser His Leu Ser Ala Leu Asn Ser Phe Gly Val Asp Glu Asn Cys
195 200 205

Trp Val Arg His Gly Ser
210

<210> 251

<211> 372

<212> DNA

<213> Mus musculus

<400> 251

gaattcgcg cgcgctcgac acagctttaa acccccatg ctcaactgtaa gggtggggcg 60
ctctgtgaaa tccacacttg gcctcccaag agcttctctca cagcctggta agccttacac 120
tcgggtgaga tgagatgata tttgtgttta ctgggtgcttc gtttttcttt atgggtcgct 180
tagaatttgt cccactctgt ttgtagtgtt ggctgtactg atgtggaaga gaaagttatg 240
cagtcctcaat cttcttatgc acagcatctc tgccctgactt tgtgggtgcct ctgttttgtg 300
cacatgcaca tgtgttcagt gttggcattg ggaatggcta tgtgcttcac caccgcttag 360
gcctggggat cc 372

<210> 252

<211> 211

<212> PRT

<213> Mus musculus

<400> 252

Gly Gln Gly Ala His Ala Gly Arg Gly Gly Ser Ser Ser Pro Met Ala
1 5 10 15

Met Pro Ala Cys Arg Ile Ser Trp Lys Trp Pro Leu Phe Trp Ile His
20 25 30

Arg Leu Cys Arg Leu Gly Gly Arg Thr Ala Ile Arg Thr Arg Trp Leu
35 40 45

Pro Val Ile Leu Arg Ala Trp Arg Arg Met Gly Pro Leu Pro Arg Ala
50 55 60

Leu Arg Tyr Arg Arg Ser Arg Phe Ala Ala His Arg Leu Leu Ser Pro
65 70 75 80

Ser Arg Val Leu Leu Asn Lys Arg Lys Ser Lys Leu Glu Phe Ala Ala
85 90 95

Ala Ser Thr Gln Leu Thr Pro His Ala His Cys Lys Val Gly Ala Leu
100 105 110

Cys Glu Ile His Thr Trp Pro Pro Lys Ser Phe Leu Thr Ala Trp Ala
115 120 125

Leu His Ser Gly Glu Met Arg Tyr Leu Cys Leu Leu Val Leu Arg Phe
130 135 140

Ser Leu Trp Val Ala Asn Leu Ser His Ser Val Cys Ser Ala Gly Cys
145 150 155 160

Thr Asp Val Glu Glu Lys Val Met Gln Ser Gln Ser Ser Tyr Ala Gln
165 170 175

His Leu Cys Leu Thr Leu Trp Cys Leu Cys Phe Val His Met His Met
180 185 190

Cys Ser Val Leu Ala Leu Gly Met Ala Met Cys Phe Thr Thr Ala Ala
195 200 205

Trp Gly Ser
210

<210> 253
<211> 689
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (62)..(85)
<223> N = A, C, G OR T/U

<400> 253
aggtaagtag tgttgactta cattaagcgc ctacatcgat ttctttcatt gaagaatata 60
cntctagtga tttttacctg gggcnttttt tgagagtgag ggtataggtg acaggttagga 120
ggagtggctg tgataagggg gactgctggt cctcctgaag ctattgatca tgccccaaga 180
agctgatgac caccatgtgt cattgaatat aaaccttggg gtttagtgag acttttgaag 240
ttaattccaa tttacctaac agactttgga tttgaagaga ctttaaactct gtctcttatt 300
acttttgtgt tttgatgtct tttcagtaat gtatcttttg tgagttaccc tagttacaaa 360
gtacctgagt aacagagtag cttcgagaca gagtacccta gtaacagagt accctagtaa 420
cagagtaccc tagagacagt acctcagtga cagagtaccc tagtgacaga tgaccctagt 480
gacagggttac ctagttacag gttaccctag tgacattggt atgttatctt tgaagataaa 540
atagttctgt gctacatgtc tttaaataat aggttaagaa ttgttctaga aatttacata 600
atgatttgca tagattagct cccatctttg ttttattcct ttgttgtttg tttgagagaa 660
gctttctgct acatcgccag agcggatcc 689

<210> 254
 <211> 209
 <212> PRT
 <213> Mus musculus

<400> 254
 Val Ser Ser Val Asp Leu His Ala Pro Thr Ser Ile Ser Phe Ile Glu
 1 5 10 15
 Glu Tyr Thr Ser Ser Asp Phe Tyr Leu Gly Xaa Phe Leu Arg Val Arg
 20 25 30
 Val Val Thr Gly Arg Arg Ser Gly Cys Asp Lys Gly Asp Cys Trp Ser
 35 40 45
 Ser Ser Tyr Ser Cys Pro Lys Lys Leu Met Thr Thr Met Cys His Ile
 50 55 60
 Thr Leu Gly Phe Ser Glu Thr Phe Glu Val Asn Ser Asn Leu Pro Asn
 65 70 75 80
 Arg Leu Trp Ile Arg Asp Phe Lys Ser Val Ser Tyr Tyr Phe Cys Val
 85 90 95
 Leu Met Ser Phe Gln Cys Ile Phe Cys Glu Leu Pro Leu Gln Ser Thr
 100 105 110
 Val Thr Glu Tyr Leu Arg Asp Arg Val Pro Gln Ser Thr Leu Val Thr
 115 120 125
 Glu Tyr Pro Arg Asp Ser Thr Ser Val Thr Glu Tyr Pro Ser Asp Arg
 130 135 140
 Pro Gln Val Thr Leu Gln Val Thr Leu Val Thr Leu Leu Cys Tyr Leu
 145 150 155 160
 Arg Asn Ser Ser Val Leu His Val Phe Lys Val Lys Asn Cys Ser Arg
 165 170 175
 Asn Leu His Asn Asp Leu His Arg Leu Ala Pro Ile Phe Val Leu Phe
 180 185 190
 Leu Cys Cys Leu Phe Glu Arg Ser Phe Leu Leu His Arg Gln Ser Gly
 195 200 205

Ser

<210> 255
 <211> 668
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (41)..(151)
 <223> N = A, C, G OR T/U

<400> 255
 gatcaaagaa ggggccttca agaacctgaa ggacttgcac ncnttgatcc nttgtcanca 60
 acaagatcag caaaatcagt ccagaggcat tcaaacctct ngtgaagttg gaaaggcttt 120
 acctgtttta gaaccaacta aaggaactgc ntgaaaaaat gcccagaact ctccaggaac 180
 ttctgtgtcca tgagaatgag atcaccaagc tgcggaaatc cgacttcaat ggactgaaca 240
 atgtgcttgc catagaactg ggcggcaacc cactgaaaaa ctctgggatt gaaaacggag 300
 ccttccaggg actgaagagt ctctcataca ttgcgcatctc agacaccaac ataactgcga 360
 tccctcaagg tctgcctact tctctcactg aagtgcacat agatggcaac aagatcacca 420
 aggttgatgc acccagcctg aaaggactga ttaatttgc taaactggga ttgagcttca 480
 acagcatcac cgttatggag aatggcagtc tggccaatgt tcctcatctg aggggaactcc 540
 acttggacaa caacaaactc ctcagggtgc ctgctgggct ggcacagcat aagtatatcc 600
 aggtcgtcta ccttcacaac aacaacatct ccgcagttgg gcaaaatgac ttctgccaaag 660
 ctggatcc 668

<210> 256
 <211> 220
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (12)..(48)
 <223> XAA = ANYTHING

<400> 256
 Ser Lys Lys Gly Pro Ser Arg Thr Arg Thr Cys Xaa Xaa Ser Xaa Val
 1 5 10 15
 Xaa Asn Lys Ile Ser Lys Ile Ser Pro Glu Ala Phe Lys Pro Leu Val
 20 25 30
 Lys Leu Glu Arg Leu Tyr Leu Phe Lys Asn Gln Leu Lys Glu Leu Xaa
 35 40 45
 Glu Lys Met Pro Arg Thr Leu Gln Glu Leu Arg Val His Glu Asn Glu
 50 55 60
 Ile Thr Lys Leu Arg Lys Ser Asp Phe Asn Gly Leu Asn Asn Val Leu
 65 70 75 80
 Val Ile Glu Leu Gly Gly Asn Pro Leu Lys Asn Ser Gly Ile Glu Asn
 85 90 95
 Gly Ala Phe Gln Gly Leu Lys Ser Leu Ser Tyr Ile Arg Ile Ser Asp
 100 105 110
 Thr Asn Ile Thr Ala Ile Pro Gln Gly Leu Pro Thr Ser Leu Thr Glu
 115 120 125

Val His Leu Asp Gly Asn Lys Ile Thr Lys Val Asp Ala Pro Ser Leu
130 135 140

Lys Gly Leu Ile Asn Leu Ser Lys Leu Gly Leu Ser Phe Asn Ser Ile
145 150 155 160

Thr Val Met Glu Asn Gly Ser Leu Ala Asn Val Pro His Leu Arg Glu
165 170 175

Leu His Leu Asp Asn Asn Lys Leu Leu Arg Val Pro Ala Gly Leu Ala
180 185 190

Gln His Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser
195 200 205

Ala Val Gly Gln Asn Asp Phe Cys Gln Ala Gly Ser
210 215 220

<210> 257

<211> 692

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (64)..(67)

<223> N = A, C, G OR T/U

<400> 257

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gactacatag gaaacgaagt ctcgaaatcc aacaataaac tcctcctcct cctcctcctc 60
ctntntntat ctcttcatat tgtaaagatc ttgtgataaa agtggttttg cttcctggat 120
tagttttatg ttttaaggta aacttggtgc ttttccctg atttatttct gagcaagttc 180
attagtatat gtggaaacgt tcctgatttg tgtatgttga aattgtatcc tgttacttta 240
cccaaagtat ttattatata taggactttt ctagttgatt ttccaagtct tttgcttttg 300
tgtataggat tacattgtct caaagtaggg ccaattttcc cttgcctttt ctatttttat 360
cccttttctt tccctgcctt atccctctaa gacatcaagc atcatcctga gtaagaaggg 420
aagaggacct cttctctcat tcctgctttt cttattgaat gtagcattga ctacagtctc 480
gtcagctata acttttattg tgtaacgta cattcttttg atgcttgtgt cacctgggct 540
tttatcagga aatgatgttg aaattaataa agaggtcttt cctcagctgc tcagacagcc 600
tctgttggag tctatctata tgcactctca cgtgtattga tttgtgtatg ttgaatcacc 660
tgtgcatccc tggaatgaaa gtaactggat cc 692
```

<210> 258

<211> 217

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (20)..(21)

<223> XAA = ANYTHING

<400> 258

Leu His Arg Lys Arg Ser Leu Glu Ile Gln Gln Thr Pro Pro Pro Pro
 1 5 10 15
 Pro Pro Pro Xaa Xaa Ile Ser Ser Tyr Cys Lys Asp Leu Val Ile Lys
 20 25 30
 Val Phe Leu Leu Pro Gly Leu Val Leu Cys Leu Arg Leu Asn Leu Leu
 35 40 45
 Leu Phe Pro Phe Ile Ser Glu Gln Val His Tyr Met Trp Lys Arg Ser
 50 55 60
 Phe Val Tyr Val Glu Ile Val Ser Cys Tyr Phe Thr Gln Ser Ile Tyr
 65 70 75 80
 Tyr Ile Asp Phe Ser Ser Phe Ser Lys Ser Phe Ala Phe Val Tyr Arg
 85 90 95
 Ile Thr Leu Ser Gln Ser Arg Ala Asn Phe Pro Leu Pro Phe Leu Phe
 100 105 110
 Leu Ser Leu Phe Phe Pro Cys Leu Ile Pro Leu Arg His Gln Ala Ser
 115 120 125
 Ser Val Arg Arg Glu Glu Asp Leu Phe Ser His Ser Cys Phe Ser Tyr
 130 135 140
 Met His Leu Gln Phe Cys Gln Leu Leu Leu Leu Cys Arg Thr Phe Phe
 145 150 155 160
 Cys Leu Cys His Leu Gly Phe Tyr Gln Glu Met Met Leu Lys Leu Ile
 165 170 175
 Lys Arg Ser Phe Leu Ser Cys Ser Asp Ser Leu Cys Trp Ser Leu Ser
 180 185 190
 Ile Cys Ile Leu Thr Cys Ile Asp Leu Cys Met Leu Asn His Leu Cys
 195 200 205
 Ile Pro Gly Met Lys Val Thr Gly Ser
 210 215

<210> 259

<211> 705

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (648)

<223> N = A, C, G OR T/U

<400> 259

cttcagcatc ttttactttc accagcgttt ctgggtggga tcccaggggtg cggatctcaa 60

gctggttgtg agagttggtg ttcaaaccac ggttgtaaac gttaaccacc gctggcgcg 120
 cgccggaac cgccagatta tagctggcag gcgtctcatc ggtactgtca aattgctggag 180
 tggaaagcgg gttaaggctg cgcagcgaag gcatggcaac cagcagaata gcgccgacaa 240
 ttaatccaat cgcaacggaa cgtaagagct tcacaaacat gatggaggcg tcattaaaaa 300
 agggaacggc agcagcatat cacgagttaa ccggacatca cacgtaagcc tgatgcccgg 360
 tttacgacat taacgcatca gcagatagat gctttcattg ccgctacaaa tttgcagggc 420
 gatgatggcc ggttttgccg ccagcacttt acgcatttca gcaatcgagt tcacccgatc 480
 gcggttgacg ccaatgatca catcgtcttt ttgcaagcca gcctgagcag ctgggcttct 540
 ttgacaactt catcgatttt aatacctttg ccgccatctt ttactgacca tcgctcaacg 600
 ttgcaccttc cagcgtggc gtgatcattt cagcgtggc cgacgaanaa gtgctggtat 660
 cgagcgtcac ttctactttc cagtgggttg ccgttacgca caagc 705

<210> 260

<211> 216

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (19)

<223> XAA = ANYTHING

<400> 260

Leu Cys Val Thr Ala Asn His Trp Lys Val Glu Val Thr Leu Asp Thr
 1 5 10 15

Ser Thr Xaa Ser Ser Ala Ser Ala Glu Met Ile Thr Pro Ala Leu Glu
 20 25 30

Gly Ala Thr Leu Ser Asp Gly Gln Lys Met Ala Ala Lys Val Leu Lys
 35 40 45

Ser Met Lys Leu Ser Lys Lys Pro Ser Cys Ser Gly Trp Leu Ala Lys
 50 55 60

Arg Arg Cys Asp His Trp Arg Gln Pro Arg Ser Gly Glu Leu Asp Cys
 65 70 75 80

Asn Ala Ser Ala Gly Gly Lys Thr Gly His His Arg Pro Ala Asn Cys
 85 90 95

Thr Arg Gln Lys His Leu Ser Ala Asp Ala Leu Met Ser Thr Gly His
 100 105 110

Gln Ala Tyr Val Cys Pro Val Asn Ser Trp Tyr Ala Ala Val Pro
 115 120 125

Phe Phe Asn Asp Ala Ser Ile Met Phe Val Lys Leu Leu Arg Ser Val
 130 135 140

Ala Ile Gly Leu Ile Val Gly Ala Ile Leu Leu Val Ala Met Pro Ser
 145 150 155 160

Leu Arg Ser Leu Asn Pro Leu Ser Thr Pro Gln Phe Asp Ser Thr Asp

165 170 175

Glu Thr Pro Ala Ser Tyr Asn Leu Ala Val Arg Arg Ala Ala Pro Ala
180 185 190

Val Val Asn Val Tyr Asn Arg Gly Leu Asn Thr Asn Ser His Asn Gln
195 200 205

Leu Glu Ile Arg Thr Leu Gly Ser
210 215

<210> 261
<211> 685
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (1)..(295)
<223> N = A, C, G OR T/U

<400> 261
ncattcctga aggacccac negatgcttt ttaantaaca agtntgcagc cattgntgnt 60
ctgcgcgagg agtccacacc tcagtcgcct ctgccacgtc tgttgccaca aagaagacag 120
agcaaggccc accatcctcc gagtacattt ttgaacggga atctaaatat ggtgcacaca 180
attaccatcc tttgcctgta gccctggaga gaggaaaagg catttatatg tgggatgtgg 240
aaggcaggca gtacttcgat ttcttgagtg cttatgggtgc tgtcagccaa ggacnctgcc 300
acccaaagat catagatgcc atgaagagtc aggtgggaca gctgacatta acatctcggg 360
ctttctataa caatgtcctt ggtgaatacg aggagtacat caccaagctt ttcaactaca 420
acaaagtctt ccctatgaat acaggagtgg aggctggaga gactgcatgt aagctcgctc 480
gtcgttgggg ctacaccgtg aaaggcatcc agaaatacaa agcaaagatt gtttttgctg 540
atgggaactt ttgggggtcga acactatctg caatctccag ttccacagat ccgaccagtt 600
atgatggctt tggacccttc atgccaggct ttgaaacctat cccatataac gatctgcccc 660
cactggagcg tgctcttcag gatcc 685

<210> 262
<211> 217
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (6)..(18)
<223> XAA = ANYTHING

<400> 262
His Ser Arg Thr Pro Xaa Asp Ala Phe Xaa Thr Ser Xaa Gln Pro Leu
1 5 10 15

Xaa Xaa Cys Ala Arg Ser Pro His Leu Ser Arg Leu Cys His Val Cys
20 25 30

Cys His Lys Glu Asp Arg Ala Arg Pro Thr Ile Leu Arg Val His Phe

5 40 45
 e Ile Trp Cys Thr Gln Leu Pro Ser Phe Ala Cys Ser Pro
 55 60
 s Arg His Leu Tyr Val Gly Cys Gly Arg Gln Ala Val
 70 75 80
 Pro Glu Cys Leu Trp Cys Cys Gln Pro Arg Thr Leu Pro
 85 90 95
 His Arg Cys His Glu Glu Ser Gly Gly Gln Ala Asp Ile
 100 105 110
 Gly Phe Leu Gln Cys Pro Trp Ile Arg Gly Val His His
 120 125
 Gln Leu Gln Gln Ser Ser Pro Tyr Glu Tyr Arg Ser Gly
 135 140
 Asp Cys Met Ala Arg Ser Ser Leu Gly Leu His Arg Glu
 150 155 160
 Glu Ile Gln Ser Lys Asp Cys Phe Cys Trp Glu Leu Leu
 165 170 175
 Thr Ile Cys Asn Leu Gln Phe His Arg Ser Asp Gln Leu
 180 185 190
 Thr Leu His Ala Arg Leu Asn His Pro Ile Arg Ser Ala
 200 205
 Ala Cys Ser Ser Gly Ser
 215

usculus

ied_base

(699)

C, G OR T/U

ttactttca ccagcgtttc tgggtgggat ccaggaatc ctgcagttcc 60
 ggggaccag gtgcccac actgcccga gcaccatcat tgctcgagc 120
 ccaggaaggc ctggtcgtcc tcgctcacca ggagccctc taggacctat 180
 ctccgttgt ctccgtgaag accattttca ccttcagtc caggagcacc 240
 tttctccat tgcgtccatc aaagcctctg tgcctttca taccagggaa 300
 ccagctgggc ctttgatacc tggaggtcca ggcagtcac gctctccagg 360
 ctctcgact ctccatcctt tccagcagga ccagctggac caagagcacc 420
 gagggcctg ctggaccagc ttgaccaggt tcaccagggg gaccttgcta 480

tccaggagaa ccaggagatc caggatgtcc agaagaacca gggggtcctg gagggcctgg 540
 tggaccagct ggtcccggat agccacccat tcttcactt cagacttgac atcatatgag 600
 tcgaattggg gagaataatt ttggccacca gttggacatg attacagatt ncangggagc 660
 caggaagccc anggagacct ggttgcctg gaanggcang gt 702

<210> 264
 <211> 220
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (2)..(18)
 <223> XAA = ANYTHING

<400> 264
 Thr Xaa Pro Phe Gln Asp Asn Gln Val Ser Xaa Gly Phe Leu Ala Pro
 1 5 10 15
 Xaa Xaa Ser Val Ile Met Ser Asn Trp Trp Pro Lys Leu Phe Ser Pro
 20 25 30
 Ile Arg Leu Ile Cys Gln Val Ser Gly Arg Met Gly Gly Tyr Pro Gly
 35 40 45
 Pro Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ser Ser Gly His
 50 55 60
 Pro Gly Ser Pro Gly Ser Pro Gly Tyr Gln Gly Pro Pro Gly Glu Pro
 65 70 75 80
 Gly Gln Ala Gly Pro Ala Gly Pro Pro Gly Pro Pro Gly Ala Leu Gly
 85 90 95
 Pro Ala Gly Pro Ala Gly Lys Asp Gly Glu Ser Gly Arg Pro Gly Arg
 100 105 110
 Pro Gly Glu Arg Gly Leu Pro Gly Pro Pro Gly Ile Lys Gly Pro Ala
 115 120 125
 Gly Met Pro Gly Phe Pro Gly Met Lys Gly His Arg Gly Phe Asp Gly
 130 135 140
 Arg Asn Gly Glu Lys Gly Glu Thr Gly Ala Pro Gly Leu Lys Gly Glu
 145 150 155 160
 Asn Gly Leu Pro Gly Asp Asn Gly Ala Pro Gly Pro Met Gly Pro Arg
 165 170 175
 Gly Ala Pro Gly Glu Arg Gly Arg Pro Gly Leu Pro Gly Ala Ala Gly
 180 185 190
 Ala Arg Gly Asn Asp Gly Ala Arg Gly Ser Asp Gly Gln Pro Gly Pro
 195 200 205

Pro Gly Pro Pro Gly Thr Ala Gly Phe Pro Gly Ser
210 215 220

<210> 265
<211> 691
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (19) .. (187)
<223> N = A, C, G OR T/U

<400> 265
tttctttgtt gctttaacnt atcaaggggt ttttgctctg cattcatgag tgcngttggg 60
tagtttttcc attgctcaca aagctttgtg tgtacaagga cttcaagaag cacgggtgcc 120
aagaaagatt tgttgctctg accttttggg gatgtttatc ccatatcttt acgggctcta 180
cctcatntgg gctgtgtttg agatgttcac tcctatcctg gaaagaagcg ggtcggagat 240
cccccccgac gttgtgctgg cctccatcct ggctgtctgt gtgatgatcc tctcttccta 300
ttttattacc ttcacttacc ttgtgaacag cacaagaaa accattctga ctctaatact 360
ggtgtgcgcg gtcaccttcc tccttgtctg cagtggagcc tttttcccat atagttctaa 420
tcccagagat ccaaagccaa agagagtgtt tcttcagcac gtgagtagaa cttttcataa 480
cttagaagga agcgtagtaa aaagagactc tggaatatgg atcaatgggt ttgattatac 540
tggaatgtct cagctaacac ctcacattcc tgagatcaac gacacaatcc gagctcactg 600
tgaggaggat gccccactct gtggttccc ttggtatctt ccagtgcact tcctgatcag 660
gaaaaactgg tatcttccaa cccccggatc c 691

<210> 266
<211> 229
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (17) .. (61)
<223> XAA = ANYTHING

<400> 266
Phe Phe Val Ala Leu Thr Tyr Gln Gly Val Phe Ala Leu His Ser Val
1 5 10 15
Xaa Leu Gly Ser Phe Ser Ile Ala His Lys Ala Leu Cys Val Gln Gly
20 25 30
Leu Gln Glu Ala Arg Cys Pro Arg Lys Ile Cys Cys Ser Asp Leu Leu
35 40 45
Gly Met Phe Ile Pro Tyr Leu Tyr Gly Leu Tyr Leu Xaa Trp Ala Val
50 55 60
Phe Glu Met Phe Thr Pro Ile Leu Glu Arg Ser Gly Ser Glu Ile Pro
65 70 75 80

Pro Asp Val Val Leu Ala Ser Ile Leu Ala Val Cys Val Met Ile Leu
85 90 95

Ser Ser Tyr Phe Ile Thr Phe Ile Tyr Leu Val Asn Ser Thr Lys Lys
100 105 110

Thr Ile Leu Thr Leu Ile Leu Val Cys Ala Val Thr Phe Leu Leu Val
115 120 125

Cys Ser Gly Ala Phe Phe Pro Tyr Ser Ser Asn Pro Glu Ser Pro Lys
130 135 140

Pro Lys Arg Val Phe Leu Gln His Val Ser Arg Thr Phe His Asn Leu
145 150 155 160

Glu Gly Ser Val Val Lys Arg Asp Ser Gly Ile Trp Ile Asn Gly Phe
165 170 175

Asp Tyr Thr Gly Met Ser His Val Thr Pro His Ile Pro Glu Ile Asn
180 185 190

Asp Thr Ile Arg Ala His Cys Glu Glu Asp Ala Pro Leu Cys Gly Phe
195 200 205

Pro Trp Tyr Leu Pro Val His Phe Leu Ile Arg Lys Asn Trp Tyr Leu
210 215 220

Pro Thr Pro Gly Ser
225

<210> 267

<211> 671

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (6)

<223> N = A, C, G OR T/U

<400> 267

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tgtttnacat attgttaaca tttttaaaaa gtgtgtgctt gtatgtatgt tgagggcatg 60
atatgtgcac aagaggcagg gcctgaaaag ggaggccagg agaaagtgtc agatacttac 120
aggggggtcac aagcctcctg ttgtagggaa tcagccttgg atcttttgca agaaccatac 180
ttgaatttaa ctggagacat ctttccagtc cctagaaatt taatttgatg ttgagtgaag 240
gttgtcaaga ttttctgtta cctatgttaa actgagtctt tgtttgtttg tttcgcacgc 300
cctcttttctt ttttaagttag cgcacagagc ggtgtgtttt gtgatgacat ttgcttgtgt 360
agttattgct gtgctttttt cttaaaccatc ctttccccag ctgacttttt ttttcccctt 420
gcttttttaat tttatatgga tttgtgtcat gatatcatgg aacgttggtg aaacactgga 480
atctagcctt ttgttttcta gattgagaac gtgaaatcca tgctaaatat ctactgacat 540
gtccacatct tgatgttggg gcagagctga gactcaaagt catcttattc aagtgtcatg 600
tgttctttat gataccatat tattaccttg tgcaatatgt aattttcatt ttgtgttttc 660
cccctggatc c
671

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<210> 268
 <211> 211
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (2)
 <223> XAA = ANYTHING

<400> 268
 Phe Xaa Ile Leu Leu Thr Phe Leu Lys Ser Val Cys Leu Tyr Val Cys
 1 5 10 15
 Gly His Asp Met Cys Thr Arg Gly Arg Ala Lys Gly Arg Pro Gly Glu
 20 25 30
 Ser Val Arg Tyr Leu Gln Gly Val Thr Ser Leu Leu Leu Gly Ile Ser
 35 40 45
 Leu Gly Ser Phe Ala Arg Thr Ile Leu Glu Phe Asn Trp Arg His Leu
 50 55 60
 Ser Ser Pro Lys Phe Asn Cys Asp Leu Ser Glu Gly Cys Gln Asp Phe
 65 70 75 80
 Leu Leu Pro Met Leu Asn Val Phe Val Cys Leu Phe Arg Thr Pro Ser
 85 90 95
 Phe Phe Leu Ser Arg Thr Glu Arg Cys Val Leu His Leu Leu Val Leu
 100 105 110
 Leu Leu Cys Phe Phe Leu Lys His Pro Phe Pro Ser Leu Phe Phe Ser
 115 120 125
 Pro Cys Phe Leu Ile Leu Tyr Gly Phe Val Ser Tyr His Gly Thr Leu
 130 135 140
 Leu Lys His Trp Asn Leu Ala Phe Cys Phe Leu Asp Glu Arg Glu Ile
 145 150 155 160
 His Ala Lys Tyr Leu Leu Thr Cys Pro His Leu Asp Val Gly Ala Glu
 165 170 175
 Leu Arg Leu Lys Val Ile Leu Phe Lys Cys His Val Phe Phe Met Ile
 180 185 190
 Pro Tyr Tyr Tyr Leu Val Gln Tyr Val Ile Phe Ile Leu Cys Phe Pro
 195 200 205
 Pro Gly Ser
 210

<210> 269
 <211> 684
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (125)..(153)
 <223> N = A, C, G OR T/U

<400> 269
 acctcagtga tgtgcaaggg tgatcaatga tcgggtgagtc tctctcatct cagtgtgtgg 60
 agtgcaagag tagagaactc agatgccaac taattcttga gcatggataa ccaaatttca 120
 ggggnaggagc cgttttcaat agctaaaagt gcntgagtta taatcacctt gtcacgtttt 180
 gggtggggttc tgaatttgca taccaaccag agcatgaaca ccagtccaca gcatatggca 240
 gcaccaaaca aaatcactcc caccatttcc ttaaagtaag aaaaagcaga ggtaagccaa 300
 gaggtaaagt ctccgagggg cactgggttcc actctgggtcc cattaaggct caggatctgc 360
 atctgcagtc tcgtctgcaa cctttccagc tcctgcgacc agttcccctt caggtaactc 420
 gatagggtctg tacttttaat aaaagaatta ttaatatacc tattgggagt aatgcacaca 480
 tgcaaaagtgg atgccacaca actcatttgt atgacatcca tcactctgttc catgtcatgt 540
 tgtaaaatat ccactctgat tcactaacat taaccctgag gtgatatgag aatccaccct 600
 ttgcagggta agcaatgcct cagacgtttt ttctgctatc tgacttatag tgtcagcagt 660
 attaatttga tctgcccttg atcc 684

<210> 270
 <211> 220
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (40)
 <223> XAA = ANYTHING

<400> 270
 Thr Ser Val Met Cys Lys Gly Asp Gln Ser Val Ser Leu Ser His Leu
 1 5 10 15
 Ser Val Trp Ser Ala Arg Val Glu Asn Ser Asp Ala Asn Phe Leu Ser
 20 25 30
 Met Asp Asn Gln Ile Ser Gly Xaa Glu Pro Phe Ser Ile Ala Lys Ser
 35 40 45
 Ala Val Ile Ile Thr Leu Ser Arg Phe Gly Trp Val Leu Asn Leu His
 50 55 60
 Thr Asn Gln Ser Met Asn Thr Ser Pro Gln His Met Ala Ala Pro Asn
 65 70 75 80
 Lys Ile Thr Pro Thr His Ser Leu Lys Glu Lys Ala Glu Val Ser Gln
 85 90 95

Glu Val Lys Ser Pro Arg Val Thr Gly Ser Thr Leu Val Pro Leu Arg
 100 105 110
 Leu Arg Ile Cys Ile Cys Ser Leu Val Cys Asn Leu Ser Ser Ser Cys
 115 120 125
 Asp Gln Phe Pro Phe Arg Leu Asp Arg Ser Val Leu Leu Ile Lys Glu
 130 135 140
 Leu Leu Ile Tyr Leu Leu Gly Val Met His Thr Cys Lys Val Asp Ala
 145 150 155 160
 Thr Gln Leu Ile Cys Met Thr Ser Ile Ile Cys Ser Met Ser Cys Cys
 165 170 175
 Lys Ile Ser Thr Leu Ile His His Pro Gly Asp Met Arg Ile His Pro
 180 185 190
 Leu Gln Gly Lys Gln Cys Leu Arg Arg Phe Phe Cys Tyr Leu Thr Tyr
 195 200 205
 Ser Val Ser Ser Ile Asn Leu Ile Cys Pro Gly Ser
 210 215 220

<210> 271
 <211> 703
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (610)..(695)
 <223> N = A, C, G OR T/U

<400> 271
 cttcagcatc ttttactttc accagcggtt ctgggtggga tcctgagcag gggctccagg 60
 ggccccagga tgcccaggcc ccatgtgtgg ggcaggtctt ctgggtgtca caggcctgtg 120
 attgctgggc ctctcctggg cagtggcccc cacacttagg agcaggatta tcacatactc 180
 gttgacggat ctgggttcct ttggagcatg tgacagagca aggccccag ggtccccact 240
 cagaccagcc acccatctct ggacagcatg gctggtcctc acaggcctgt agctgccact 300
 caagagttcc aggagccaca ttctcagagc actgaccacc tctgcccaca cagcgctgtg 360
 gtcgcagctg ggacccctca gaacatgtaa ctgagcaggg ccccccataag gaccatgctg 420
 accattgtgg agacctgcat gcctgacaga ggccaccatc atgctcctgg aaggcatagg 480
 cagcgttgag acagcagtct tctaccctga tgtctctccc aagtaggctt ttgcacctgc 540
 cagaggactc ctcatactgg gtgaagcaaa gcacaggggtc tgagcctgtg gctggcagga 600
 taaccagtan cagcaggagc cactgagggg cttgcatttc ancangcatt ttgaacacta 660
 tgtttctgca ctcctacaaa aaagangcgt cnacnccggc cgc 703

<210> 272
 <211> 221
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (19)..(31)
 <223> XAA = ANYTHING

<400> 272

Ala Ala Gly Val Asp Ala Ser Phe Leu Glu Cys Arg Asn Ile Val Phe
 1 5 10 15

Lys Met Xaa Xaa Glu Met Gln Ala Pro Gln Trp Leu Leu Leu Xaa Leu
 20 25 30

Val Ile Leu Pro Ala Thr Gly Ser Asp Pro Val Leu Cys Phe Thr Gln
 35 40 45

Tyr Glu Glu Ser Ser Gly Arg Cys Lys Gly Leu Leu Gly Arg Asp Ile
 50 55 60

Arg Val Glu Asp Cys Cys Leu Asn Ala Ala Tyr Ala Phe Gln Glu His
 65 70 75 80

Asp Gly Gly Leu Cys Gln Ala Cys Arg Ser Pro Gln Trp Ser Ala Trp
 85 90 95

Ser Leu Trp Gly Pro Cys Ser Val Thr Cys Ser Glu Gly Ser Gln Leu
 100 105 110

Arg His Arg Arg Cys Val Gly Arg Gly Gly Gln Cys Ser Glu Asn Val
 115 120 125

Ala Pro Gly Thr Leu Glu Trp Gln Leu Gln Ala Cys Glu Asp Gln Pro
 130 135 140

Cys Cys Pro Glu Met Gly Gly Trp Ser Glu Trp Gly Pro Trp Gly Pro
 145 150 155 160

Cys Ser Val Thr Cys Ser Lys Gly Thr Gln Ile Arg Gln Arg Val Cys
 165 170 175

Asp Asn Pro Ala Pro Lys Cys Gly Gly His Cys Pro Gly Glu Ala Gln
 180 185 190

Gln Ser Gln Ala Cys Asp Thr Gln Lys Thr Cys Pro Thr His Gly Ala
 195 200 205

Trp Ala Ser Trp Gly Pro Trp Ser Pro Cys Ser Gly Ser
 210 215 220

<210> 273
 <211> 685
 <212> DNA
 <213> Mus musculus

<220>

<221> modified_base
 <222> (10)..(78)
 <223> N = A, C, G OR T/U

<400> 273
 aaaaaaagtn aagttggcct tgtgctgaac ggccaaccca ctgaaagtag aagtgcggt 60
 tcgataccag cacttnttng tcggccagcg ttgaaatgat cacgccagcg tggaagggtgc 120
 aacgttgagc gatggtcagc taaaagatgg cggcaaagggt attaaaatcg atgaagttgt 180
 caaagaagcc cagctgctca ggctggcttg caaaaagacg atgtgatcat tggcgtcaac 240
 cgcgatcggg tgaactcgat tgctgaaatg cgtaaagtgc tgcggcaaaa ccggccatca 300
 tcgccctgca aattgtacgc ggcaatgaaa gcattctatct gctgatgcgt taatgtcgta 360
 aaccgggcat caggcttacg tgtgatgtcc ggtaactcg tggtatgctg ctgccgttcc 420
 cttttttaat gacgcctcca tcatgtttgt gaagctctta cgttccgttg cgattggatt 480
 aattgtcggc gctattctgc tggttgccat gccttcgctg cgcagcctta acccgcttcc 540
 cactccgcaa tttgacagta ccgatgagac gcctgccagc tataatctgg cggttcgccg 600
 cgccgcgcca gcggtggtta acgtttacaa ccgtggtttg aacaccaact ctcaacca 660
 gcttgagatc cgcaccctgg gatcc 685

<210> 274
 <211> 222
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (25)
 <223> XAA = ANYTHING

<400> 274
 Lys Lys Val Lys Leu Ala Leu Cys Val Thr Ala Asn Pro Leu Lys Val
 1 5 10 15
 Glu Val Thr Val Arg Tyr Gln His Xaa Xaa Val Gly Gln Arg Asn Asp
 20 25 30
 His Ala Ser Val Glu Gly Ala Thr Leu Ser Asp Gly Gln Leu Lys Asp
 35 40 45
 Gly Gly Lys Gly Ile Lys Ile Asp Glu Val Val Lys Glu Ala Gln Leu
 50 55 60
 Leu Arg Leu Ala Cys Lys Lys Thr Met Ser Leu Ala Ser Thr Ala Ile
 65 70 75 80
 Gly Thr Arg Leu Leu Lys Cys Val Lys Cys Cys Gly Lys Thr Gly His
 85 90 95
 His Arg Pro Ala Asn Cys Thr Arg Gln Lys His Leu Ser Ala Asp Ala
 100 105 110
 Leu Met Ser Thr Gly His Gln Ala Tyr Val Cys Pro Val Asn Ser Trp
 115 120 125
 Tyr Ala Ala Ala Val Pro Phe Phe Asn Asp Ala Ser Ile Met Phe Val

130	135	140
Lys Leu Leu Arg Ser Val Ala Ile Gly Leu Ile Val Gly Ala Ile Leu		
145	150	155 160
Leu Val Ala Met Pro Ser Leu Arg Ser Leu Asn Pro Leu Ser Thr Pro		
	165	170 175
Gln Phe Asp Ser Thr Asp Glu Thr Pro Ala Ser Tyr Asn Leu Ala Val		
	180	185 190
Arg Arg Ala Ala Pro Ala Val Val Asn Val Tyr Asn Arg Gly Leu Asn		
	195	200 205
Thr Asn Ser His Asn Gln Leu Glu Ile Arg Thr Leu Gly Ser		
	210	215 220

<210> 275
 <211> 703
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (656)..(698)
 <223> N = A, C, G OR T/U

<400> 275
 cttcagcatc ttttactttc accagcgttt ctgggtggga tccctgttcc tgactgtctg 60
 agatgaggct tagccaactc tgttcctgag tgaatctgcc cagcagatag ttaatagtaa 120
 tccaccata ggcaccttcc tcttgtccag tgatgatctt ggcaccctgg aagtcaaagg 180
 ggtagctctt aaggttgggt gacactgcag ccaggacctc gtctgccgat tgttcgcttt 240
 ccattctaag caagcgcagt cctgctgtgg ctcccaggta gacaggagtc tggatgatgt 300
 tggatgttgg tatcagttcg gtggacagtt ccatgcattc ggccagggtac gcaccgattt 360
 catctgtttt ctgagcatat tttgagattc caggaccttt cacttggcat tcctctaact 420
 gctgcaccac cctgtgtca ttctccttct cggccggcca cttgtagatg tacaggttgg 480
 tgtgagatga ccccgcatcc aacacaatcc catacttaac attttctggc aaaggtttgt 540
 tctgggtcag tcccacagca atcaaagcta tcacagccaa gatagagggtg aaaccaagga 600
 tgatcaagaa tatttttggg gcaaaatctc ttcaccttag aatcctttat atcttncata 660
 aggggcaagc tttttgggtc ctttctcttc ctcgctgnct tgg 703

<210> 276
 <211> 220
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (2)..(7)
 <223> XAA = ANYTHING

<400> 276
 Pro Xaa Gln Arg Gly Arg Xaa Arg Asn Gln Lys Ala Cys Pro Leu Xaa

1	5	10	15
Lys Ile Arg Ile Leu Arg Arg Asp Phe Ala Pro Lys Ile Phe Leu Ile	20	25	30
Ile Leu Gly Phe Thr Ser Ile Leu Ala Val Ile Ala Leu Ile Ala Val	35	40	45
Gly Leu Thr Gln Asn Lys Pro Leu Pro Glu Asn Val Lys Tyr Gly Ile	50	55	60
Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu Tyr Ile Tyr Lys Trp	65	70	75
Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val Gln Gln Leu Glu Glu	85	90	95
Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr Ala Gln Lys Thr Asp	100	105	110
Glu Ile Gly Ala Tyr Leu Ala Glu Cys Met Glu Leu Ser Thr Glu Leu	115	120	125
Ile Pro Thr Ser Lys His His Gln Thr Pro Val Tyr Leu Gly Ala Thr	130	135	140
Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Gln Ser Ala Asp Glu	145	150	155
Val Leu Ala Ala Val Ser Thr Ser Leu Lys Ser Tyr Pro Phe Asp Phe	165	170	175
Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp	180	185	190
Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr Gln Glu Gln Ser Trp	195	200	205
Leu Ser Leu Ile Ser Asp Ser Gln Glu Gln Gly Ser	210	215	220

<210> 277

<211> 719

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (628)..(666)

<223> N = A, C, G OR T/U

<400> 277

cttcagcatc ttttctttca ccagcgtttc tgggtgggat ccaggggtgg ggtggaaaac 60
 ttgctaaaaa caagcaaat gtctttcaat attcacaacc ttaaattat atccaagaaa 120

acaaaggata aataattttt tataaaaata attacttctc aaataacggt tcacaataga 180
 cctgctcaat acatcgatct gactcatctc atctgtgccg cttttcttct ttttaaaatt 240
 ctggcctggg acaaaactac atgaaagaaa gtaccattaa attaagggtt actttccaaa 300
 aaacaataga aaaatcttaa agtaaatctt acttatatat aaaatattaa ggcctctgca 360
 tgagaacggt ttaacatctg gggaactggc ctttcctaac tgacctatga cccactcac 420
 ctcaaacttc agaatgaaag gttctggagt gaaaagtctt ttttaatttg ccaatacatg 480
 aaattacaca taaaattaca ctgcaaagta atatgtactt aacaaatgat atattgaaaa 540
 gtctaacttt ctgctggcta atttcagtat ggacttcaga tcaagtatag tgtattttca 600
 gccatatctc ataatctttt gcgacgcngn cgcgaattca agcttactct tnccttttca 660
 attcanaaga actcgtcaag aaggcgatag aaggcgatgc gctgcgaatc gggagccgg 719

<210> 278
 <211> 219
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (17)..(28)
 <223> XAA = ANYTHING

<400> 278
 Gly Ser Arg Phe Ala Ala His Arg Leu Leu Ser Pro Ser Arg Val Leu
 1 5 10 15
 Xaa Asn Lys Xaa Lys Ser Lys Leu Glu Phe Ala Xaa Ala Ser Gln Lys
 20 25 30
 Ile Met Arg Tyr Gly Lys Tyr Thr Ile Leu Asp Leu Lys Ser Ile Leu
 35 40 45
 Lys Leu Ala Ser Arg Lys Leu Asp Phe Ser Ile Tyr His Leu Leu Ser
 50 55 60
 Thr Tyr Tyr Phe Ala Val Phe Tyr Val Phe His Val Leu Ala Lys Leu
 65 70 75 80
 Lys Gly Leu Phe Thr Pro Glu Pro Phe Ile Leu Lys Phe Glu Val Ser
 85 90 95
 Gly Val Ile Gly Gln Leu Gly Lys Ala Ser Ser Pro Asp Val Lys Pro
 100 105 110
 Phe Ser Cys Arg Gly Leu Asn Ile Leu Tyr Ile Ser Glu Phe Thr Phe
 115 120 125
 Lys Ile Phe Leu Leu Phe Phe Gly Lys Pro Leu Ile Trp Tyr Phe Leu
 130 135 140
 Ser Cys Ser Phe Val Pro Gly Gln Asn Phe Lys Lys Lys Lys Ser Gly
 145 150 155 160
 Thr Asp Glu Met Ser Gln Ile Asp Val Leu Ser Arg Ser Ile Val Lys
 165 170 175

Arg Tyr Leu Arg Ser Asn Tyr Phe Tyr Lys Lys Leu Phe Ile Leu Cys
 180 185 190

Phe Leu Gly Tyr Asn Phe Lys Val Val Asn Ile Glu Arg His Leu Leu
 195 200 205

Cys Phe Gln Val Phe His Pro Thr Pro Gly Ser
 210 215

<210> 279

<211> 703

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (582)..(701)

<223> N = A, C, G OR T/U

<400> 279

cttcgcatct tttactttcc cagcggttct ggggtgggatc cagcagcaag ttccaccatg 60
 atgctctcac cattctttgt gatgaaaggt gtgatgaaga caaagaacac atcgtagatg 120
 agaagaaggc ctagcagtat cagcgtatgac atgaaattgg gtaacttcat tgttttaatt 180
 aagttgagac agaaagcaat tcctaagata tcctgtaaaa tccaagcca cctatcctca 240
 tttcgaaata cagccacac aacagcaact gagatgcaca gcccggaag gaaaatcagg 300
 ctcactttaa tgtttttgcc acaacacaaa atcgtgcact gtccacatgg catcctatga 360
 atcaatgcag aaagacagtt gtacaggctc attgacgatg ctatgcagaa aatcgctatc 420
 ataacatata caagccacct gtagaagaaa tacagtaaga caatgtcgac gcggccgcga 480
 attcaagctt actcttcctt tttcaattca gaagaactcg tcaagaaggc gatagaaggc 540
 gatgcgctgc gaatcgggag cggcgatacc gtaaagcacg angaagcggg caggccattc 600
 gccgncaagc tcttcacaat atcacgggta gncaacgcta tgtcctgata gcgggtccgnc 660
 acaccagacc cggncacagt cgatgaatnc agaaaagcgg nct 703

<210> 280

<211> 220

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (1)..(33)

<223> XAA = ANYTHING

<400> 280

Xaa Ala Phe Leu Xaa Ser Ser Thr Val Xaa Gly Leu Gly Val Xaa Asp
 1 5 10 15

Arg Tyr Gln Asp Ile Ala Leu Xaa Thr Arg Asp Ile Val Lys Ser Leu
 20 25 30

Xaa Ala Asn Gly Leu Thr Ala Ser Ser Cys Phe Thr Val Ser Pro Leu
 35 40 45

Pro Ile Arg Ser Ala Ser Pro Ser Ile Ala Phe Leu Thr Ser Ser Ser
 50 55 60
 Glu Leu Lys Lys Glu Glu Ala Ile Arg Gly Arg Val Asp Ile Val Leu
 65 70 75 80
 Leu Tyr Phe Phe Tyr Arg Trp Leu Val Tyr Val Met Ile Ala Ile Phe
 85 90 95
 Cys Ile Ala Ser Ser Met Ser Leu Tyr Asn Cys Leu Ser Ala Leu Ile
 100 105 110
 His Arg Met Pro Cys Gly Gln Cys Thr Ile Leu Cys Cys Gly Lys Asn
 115 120 125
 Ile Lys Val Ser Leu Ile Phe Leu Ser Gly Leu Cys Ile Ser Val Ala
 130 135 140
 Val Val Trp Ala Val Phe Arg Asn Glu Asp Arg Trp Ala Trp Ile Leu
 145 150 155 160
 Gln Asp Ile Leu Gly Ile Ala Phe Cys Leu Asn Leu Ile Lys Thr Met
 165 170 175
 Lys Leu Pro Asn Phe Met Ser Cys Val Ile Leu Leu Gly Leu Leu Leu
 180 185 190
 Ile Tyr Asp Val Phe Phe Val Phe Ile Thr Pro Phe Ile Thr Lys Asn
 195 200 205
 Gly Glu Ser Ile Met Val Glu Leu Ala Ala Gly Ser
 210 215 220

<210> 281

<211> 722

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (698)

<223> N = A, C, G OR T/U

<400> 281

cttcagcatc ttttactttc accagcggtt ctgggtggga tcctgtcgat gtgacccat 60
 gactaggtaa gtgtggttca actttaacgt aaatatcatt cttccagaca tatgccaact 120
 tatgaccttc tggtagccat gtgatccact gtgtattatt tggaaatctt tcttctgtga 180
 tcagctgtct tttattcaca tcataaatgt tgtatgaagc tgtgtaggaa tgtctccatt 240
 gcttcacgta gttgtattcc aagagaacaa acagtcgggc aggtgacact gaatgatatc 300
 caaagctttc aaaggtagtg ttctccaaga aaatggagct gtttccatgt tcagcattga 360
 gcagcaagat attgttctct tgtttgtaga ggtattcaaa gtctgaaacc caccacaaag 420
 agtaggactt gacccgaaag gtactcttta aatagtcagc tagtgaatac gttctgcggc 480
 tgtcagctgc cgcttcatct ttgctcagca gaactattgg cacggtgatg atggtgacaa 540

gcgcagcgac accaagcagt cccagaagaa ccttcacgg tgtcttcatg gtcgggcccgc 600
tccttgaaac tgaactctga agcttgagcg cagcagaagt cactgcgcgc agagacggac 660
gtccgtcgac gccggccgcg aattcaagct tactcttntc ttttcaattc agaagaactc 720
gt 722

<210> 282

<211> 227

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (7)

<223> XAA = ANYTHING

<400> 282

Arg Val Leu Leu Asn Lys Xaa Lys Ser Lys Leu Glu Phe Ala Ala Gly
1 5 10 15
Val Asp Gly Arg Pro Ser Leu Arg Ala Val Thr Ser Ala Ala Leu Lys
20 25 30
Leu Gln Ser Ser Val Ser Arg Ser Arg Pro Thr Met Lys Thr Pro Trp
35 40 45
Lys Val Leu Leu Gly Leu Leu Gly Val Ala Ala Leu Val Thr Ile Ile
50 55 60
Thr Val Pro Ile Val Leu Leu Ser Lys Asp Glu Ala Ala Ala Asp Ser
65 70 75 80
Arg Arg Thr Tyr Ser Leu Ala Asp Tyr Leu Lys Ser Thr Phe Arg Val
85 90 95
Lys Ser Tyr Ser Leu Trp Trp Val Ser Asp Phe Glu Tyr Leu Tyr Lys
100 105 110
Gln Glu Asn Asn Ile Leu Leu Leu Asn Ala Glu His Gly Asn Ser Ser
115 120 125
Ile Phe Leu Glu Asn Ser Thr Phe Glu Ser Phe Gly Tyr His Ser Val
130 135 140
Ser Pro Asp Arg Leu Phe Val Leu Leu Glu Tyr Asn Tyr Val Lys Gln
145 150 155 160
Trp Arg His Ser Tyr Thr Ala Ser Tyr Asn Ile Tyr Asp Val Asn Lys
165 170 175
Arg Gln Leu Ile Thr Glu Glu Lys Ile Pro Asn Asn Thr Gln Trp Ile
180 185 190
Thr Trp Ser Pro Glu Gly His Lys Leu Ala Tyr Val Trp Lys Asn Asp
195 200 205

Ile Tyr Val Lys Val Glu Pro His Leu Pro Ser His Arg Ile Thr Ser
 210 215 220

Thr Gly Ser
 225

<210> 283
 <211> 701
 <212> DNA
 <213> Mus musculus
 <220>
 <221> modified_base
 <222> (558)..(701)
 <223> N = A, C, G OR T/U

<400> 283
 cttcagcatc ttttactttc accagcgttt ctgggtggga tccgtttctt ttctctaaat 60
 ctttaattct gaactggcct tgagcgggct tgctttcctt gtctttatag taggcaatga 120
 gttgaactgt gtagttctgc tctggcagaa ggccttgaat aatcgctttt gttgcagtgt 180
 tctggagatt catctggttg gtctttcctc ctgaagctgg agccacgagc agtttgtagc 240
 caccaaattt cctcttgggt gctttccatg aaatctgtat actatcatgg gaaatcacat 300
 tatactttaa ccttgtgggt ggagccactt gtcccctgac aatggtgcag aaacaagcag 360
 ccgcaaaaaa agctagaatc agccagtccc gcatcttgca ctgccaaatc atcatcttat 420
 tttctgcctc ttacatcagg tgcaacagct gcctgtgcag ggcaacgttc cagcccaggt 480
 tggggacctc ttggcgcccta gggaagatta agtcgacgag gccgcgaatt caagcttact 540
 cttccttttt caattcanaa gaactcgta agaangcgat agaaggcgat gcgctgcgaa 600
 tcgggagcgg cgatcccgt aagcacgagg aagcggncag cccattcgcc gncaagctct 660
 tnagcaatat cacgggtagc caacgctatg tncatgatagc n 701

<210> 284
 <211> 217
 <212> PRT
 <213> Mus musculus
 <220>
 <221> MOD_RES
 <222> (3)..(47)
 <223> XAA = ANYTHING

<400> 284
 Ala Ile Xaa Thr Arg Trp Leu Pro Val Ile Leu Leu Lys Ser Leu Xaa
 1 5 10 15
 Ala Asn Gly Leu Xaa Ala Ser Ser Cys Phe Thr Gly Ser Pro Leu Pro
 20 25 30
 Ile Arg Ser Ala Ser Pro Ser Ile Ala Phe Leu Thr Ser Ser Xaa Glu
 35 40 45
 Leu Lys Lys Glu Glu Ala Ile Arg Gly Arg Val Asp Leu Ile Phe Pro
 50 55 60

Arg Arg Gln Glu Val Pro Asn Leu Gly Trp Asn Val Ala Leu His Arg
65 70 75 80

Gln Leu Leu His Leu Met Glu Ala Glu Asn Lys Met Met Ile Trp Gln
85 90 95

Cys Lys Met Arg Asp Trp Leu Ile Leu Ala Phe Leu Ala Ala Ala Cys
100 105 110

Phe Cys Thr Ile Val Arg Gly Gln Val Ala Pro Pro Thr Arg Leu Arg
115 120 125

Tyr Asn Val Ile Ser His Asp Ser Ile Gln Ile Ser Trp Lys Ala Pro
130 135 140

Arg Gly Lys Phe Gly Gly Tyr Lys Leu Leu Val Ala Pro Ala Ser Gly
145 150 155 160

Gly Lys Thr Asn Gln Met Asn Leu Gln Asn Thr Ala Thr Lys Ala Ile
165 170 175

Ile Gln Gly Leu Leu Pro Glu Gln Asn Tyr Thr Val Gln Leu Ile Ala
180 185 190

Tyr Tyr Lys Asp Lys Glu Ser Lys Pro Ala Gln Gly Gln Phe Arg Ile
195 200 205

Lys Asp Leu Glu Lys Arg Asn Gly Ser
210 215

<210> 285

<211> 723

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (600)..(707)

<223> N = A, C, G OR T/U

<400> 285

cttcgcatct tttactttca ccagcgtttc tgggtgggat ccgagcataa ataagacaga 60
gaaaatccat ggatataagt attcttgag gcaacaccac atagacattt agaaaattac 120
ttaagtgttt tttgaatttt tactttacat gacttcatta attgtacttc cattaaagaa 180
gagtttgtaa cacatctgta aacaaaaaag gcatatagca ttctattctt aatgaagaaa 240
gaacatattt aaccacaaag taaaggaata atcacaataa aaagaagagc ttagtctcat 300
gaatatatat attgagtga tgaataaata tatggtcgac gcggccgcca attcaagctt 360
actcttcctt tttcaattca gaagaactcg tcaagaaggc gatagaaggc gatgcgctgc 420
gaatcgggag cggcgatacc gtaaagcagc aggaagcggc cagcccatc gccgccaagc 480
tcttcagcaa tatcacgggt agccaacgct atgtcctgat agcggtcgcg cacaccacgc 540
cggccacagt cgatgaatcc agaaaagcgg ccattttcca ccatgatatt cggcaagcan 600
gcatcgccat gggtcacgac gagatcctcg ccgtcgggca tgcgcgcctt gagcctggcg 660
aacagttcgg ctggcgcgag cccctgatgc tcttcgtcca gatcatnctg atcggcaaga 720

<210> 286

<211> 217

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (6) .. (41)

<223> XAA = ANYTHING

<400> 286

Arg Ser Cys Arg Ser Xaa Ser Gly Arg Arg Ala Ser Gly Ala Arg Ala
 1 5 10 15

Ser Arg Thr Val Arg Gln Ala Gln Gly Ala His Ala Arg Arg Arg Gly
 20 25 30

Ser Arg Arg Asp Pro Trp Arg Cys Xaa Leu Ala Glu Tyr His Gly Gly
 35 40 45

Lys Trp Pro Leu Phe Trp Ile His Arg Leu Trp Pro Ala Gly Cys Gly
 50 55 60

Gly Pro Leu Ser Gly His Ser Val Gly Tyr Pro Tyr Cys Arg Ala Trp
 65 70 75 80

Arg Arg Met Gly Pro Leu Pro Arg Ala Leu Arg Tyr Arg Arg Ser Arg
 85 90 95

Phe Ala Ala His Arg Leu Leu Ser Pro Ser Arg Val Leu Leu Asn Lys
 100 105 110

Arg Lys Ser Lys Leu Glu Phe Ala Ala Ala Ser Thr Ile Tyr Leu Phe
 115 120 125

Ile His Ser Ile Tyr Ile Phe Met Ser Ser Ser Ser Phe Tyr Cys Asp
 130 135 140

Tyr Ser Phe Thr Leu Trp Leu Asn Met Phe Phe Leu His Glu Asn Ala
 145 150 155 160

Ile Cys Leu Phe Cys Leu Gln Met Cys Tyr Lys Leu Phe Phe Asn Gly
 165 170 175

Ser Thr Ile Asn Glu Val Met Ser Lys Asn Ser Lys Asn Thr Val Ile
 180 185 190

Phe Met Ser Met Trp Cys Cys Leu Gln Glu Tyr Leu Tyr Pro Trp Ile
 195 200 205

Phe Ser Val Leu Phe Met Leu Gly Ser
 210 215

<210> 287
 <211> 705
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> (655)
 <223> N = A, C, G OR T/U

<400> 287
 cttcagcatc ttttactttc accagcggtt ctgggtggga tccgggggtgt gttactggca 60
 tctatggagt agatgtaagt aatgttgata aacagcctat aatgcacagc atagcctgac 120
 ccccaaaaga agtatacatc ccagaatata aatggtacag agattgagaa aactctcatt 180
 gagggcctag ttgtatttct tgttcaagac aagggttaca catttcaatt aagagagttc 240
 agctctacaa agaagtttta gtcgacgcgg ccgcgaattc aagcttactc ttcctttttc 300
 aattcagaag aactcgtcaa gaaggcgata gaaggcgatg cgctgcgaat cgggagcggc 360
 gataccgtaa agcacgagga agcggtcagc ccattcgccg ccaagctctt cagcaatata 420
 acgggtagcc aacgctatgt cctgatagcg gtccgccaca cccagccggc cacagtcgat 480
 gaatccagaa aagcggccat tttccaccat gatattcggc aagcaggcat cgccatgggt 540
 cagcagcaga tctcgcctgt cgggcatgcg cgccttgagc ctggcgaaca gttcggctgg 600
 cgcgagcccc tgatgctctt cgtccagatc atcctgatcg acaaagaccg gcttncatcc 660
 gagtacgtgc tcgctcgatg cgatgtttcg cttgggtggtc gaatg 705

<210> 288
 <211> 222
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (17)
 <223> XAA = ANYTHING

<400> 288
 Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala Arg Thr Arg Met
 1 5 10 15

 Xaa Ala Gly Leu Cys Arg Ser Gly Ser Gly Arg Arg Ala Ser Gly Ala
 20 25 30

 Arg Ala Ser Arg Thr Val Arg Gln Ala Gln Gly Ala His Ala Arg Arg
 35 40 45

 Arg Gly Ser Arg Arg Asp Pro Trp Arg Cys Leu Leu Ala Glu Tyr His
 50 55 60

 Gly Gly Lys Trp Pro Leu Phe Trp Ile His Arg Leu Trp Pro Ala Gly
 65 70 75 80

 Cys Gly Gly Pro Leu Ser Gly His Ser Val Gly Tyr Pro Tyr Cys Arg
 85 90 95

Ala Trp Arg Arg Met Gly Pro Leu Pro Arg Ala Leu Arg Tyr Arg Arg
100 105 110

Ser Arg Phe Ala Ala His Arg Leu Leu Ser Pro Ser Arg Val Leu Leu
115 120 125

Asn Lys Arg Lys Ser Lys Leu Glu Phe Ala Ala Ala Ser Thr Lys Thr
130 135 140

Ser Leu Ser Thr Leu Leu Ile Glu Met Leu Pro Cys Leu Glu Gln Glu
145 150 155 160

Ile Gln Leu Gly Pro Gln Glu Phe Ser Gln Ser Leu Tyr His Tyr Ser
165 170 175

Gly Met Tyr Thr Ser Phe Gly Gly Gln Ala Met Leu Cys Ile Ile Gly
180 185 190

Cys Leu Ser Thr Leu Leu Thr Ser Thr Pro Met Pro Val Thr His Pro
195 200 205

Gly Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu
210 215 220

<210> 289

<211> 722

<212> DNA

<213> Mus musculus

<220>

<221> modified base

<222> (702)..(722)

<223> N = A, C, G OR T/U

<400> 289

cttcagcatc ttttactttc accagcggtt ctgggtggga tcccaggagt tttccttcgc 60
tgataaaggg ttctgggaag caggtagcag cagagatggt acagacagca tctcccat 120
agaaaataca cccattatc atcatttttc caaacgagg ttcaatgggg agtttagcca 180
ggattcgtcc aagaggagtc aactcatcat tggcatctaa agcatcaagt tctcttagag 240
tatgctctgc ttcaattaca gcatccaaag gtggagggtc gattgccttt gcaaggaatt 300
ggccaattcc tcttagacgc agaagtttta tgctcagagc aatttcatgc aatggtgttc 360
taaacatctc tgggtgtcatg tgggtctcta gtctaaaatt tagaagtaga aaagtcaaac 420
atgacaacat aacaaaaatc tttgcataaa aaaactgggt attatagtgg ccctttccta 480
gtctatacca cacaactttt cctattgact acaaaactag actagttgac tgaaaactgg 540
ctcctgactt tactttcaca gccagggtat cttttaactg ataagtagag gagtaaggaa 600
aaaagttaat gctaacactt ctaactatgg ctactaccta cggatcctac ctattaacaa 660
gcacggacaa caacaaaacg ggcccaaact cagcaaaagg cnggacataa atataataaa 720
cn 722

<210> 290

<211> 237

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (7)

<223> XAA = ANYTHING

<400> 290

Val Tyr Tyr Ile Tyr Val Xaa Pro Phe Ala Glu Phe Gly Pro Val Leu
1 5 10 15

Leu Leu Ser Val Leu Val Asn Arg Asp Arg Val Val Ala Ile Val Arg
20 25 30

Ser Val Ser Ile Asn Phe Phe Pro Tyr Ser Ser Thr Tyr Gln Leu Lys
35 40 45

Asp Thr Leu Ala Val Lys Val Lys Ser Gly Ala Ser Phe Gln Ser Thr
50 55 60

Ser Leu Val Leu Ser Ile Gly Lys Val Val Trp Tyr Arg Leu Gly Lys
65 70 75 80

Gly His Tyr Asn Thr Gln Phe Phe Tyr Ala Lys Ile Phe Val Met Leu
85 90 95

Ser Cys Leu Thr Phe Leu Leu Leu Asn Phe Arg Leu Glu Thr His Met
100 105 110

Thr Pro Glu Met Phe Arg Thr Pro Leu His Glu Ile Ala Leu Ser Ile
115 120 125

Lys Leu Leu Arg Leu Gly Gly Ile Gly Gln Phe Leu Ala Lys Ala Ile
130 135 140

Glu Pro Pro Pro Leu Asp Ala Val Ile Glu Ala Glu His Thr Leu Arg
145 150 155 160

Glu Leu Asp Ala Leu Asp Ala Asn Asp Glu Leu Thr Pro Leu Gly Arg
165 170 175

Ile Leu Ala Lys Leu Pro Ile Glu Pro Arg Phe Gly Lys Met Met Ile
180 185 190

Met Gly Cys Ile Phe Tyr Val Gly Asp Ala Val Cys Thr Ile Ser Ala
195 200 205

Ala Thr Cys Phe Pro Glu Pro Phe Ile Ser Glu Gly Lys Leu Leu Gly
210 215 220

Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu
225 230 235

<210> 291

<211> 703
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (547)..(702)
<223> N = A, C, G OR T/U

<400> 291
cttcagcatc ttttactttc accagcggtt ctgggtggga tccactcttg ctacccaact 60
gtttgtggaa gaaagtctgg agctgctgcc atgcgtccac ctgggccacg gcatgagccc 120
tgggctcccc tccaaagggtg atgttggcac ccaccaggag gtgcatgcca gcgctgcaca 180
gcgggaagta agggggctcg atgtaatgcc ctgctgctgg gtagcagatg atctggggct 240
tctccttccc gtgcgcctgc aggcgtttgg agatctcatc agcatagaac tcgctcttcc 300
agttgtggtc gtctgacct acgaggaaca ggaaggctgt gtcagacctt tccacgggaa 360
tgaagctctt cttgtctacc agagggcttt gcagagcttc caccgacatcc aagagaccat 420
ctttggatcat ttgacttgg tttctcagaa gggacacagg gggatatagtc tcatccttgt 480
aggagatggg gttcccaaca gcagccacgg agccattgat gaccacagca gctgtgatgc 540
ccttcangaa ggaggccata ncaaggccaa gttcaccccc tttggaaatc ccaagcagcc 600
caattccagg tccttttacc tcgggggtggc tgcgcangta gttcacggct tcttcaaagt 660
actccatgtg catgggttct atgctcttgg ggaaggctgt cnt 703

<210> 292
<211> 703
<212> DNA
<213> Mus musculus

<220>
<221> modified_base
<222> (695)
<223> N = A, C, G OR T/U

<400> 292
cttcagcatc ttttactttc accagcggtt ctgggtggga tccactcttg ctacccaact 60
gtttgtggaa gaaagtctgg agctgctgcc atgcgtccac ctgggccacg gcatgagccc 120
tgggctcccc tccaaagggtg atgttggcac ccaccaggag gtgcatgcca gcgctgcaca 180
gcgggaagta agggggctcg atgtaatgcc ctgctgctgg gtagcagatg atctggggct 240
tctccttccc gtgcgcctgc aggcgtttgg agatctcatc agcatagaac tcgctcttcc 300
agttgtggtc gtctgacct acgaggaaca ggaaggctgt gtcagacctt tccacgggaa 360
tgaagctctt cttgtctacc agagggcttt gcagagcttc caccgacatcc aagagaccat 420
ctttggatcat ttgacttgg tttctcagaa gggacacagg gggatatagtc tcatccttgt 480
aggagatggg gttcccaaca gcagccacgg agccattgat gaccacagca gctgtgatgc 540
ccttcaggaa ggaggccata gcaaggccaa gttcaccccc tttggaaatc ccaagcagcc 600
caattccagg tccttttacc tcgggggtggc tgcgcaggta gttcacggct tcttcaaaag 660
tactccatgt gcatgggttc tatgctcttg gggangtctg cgt 703

<210> 293
<211> 231
<212> PRT
<213> Mus musculus

<400> 293

Thr Ser Pro Arg Ala Lys Pro Cys Thr Trp Ser Thr Phe Glu Glu Ala
 1 5 10 15
 Val Asn Tyr Leu Arg Ser His Pro Glu Val Lys Gly Pro Gly Ile Gly
 20 25 30
 Leu Leu Gly Ile Ser Lys Gly Gly Glu Leu Gly Leu Ala Met Ala Ser
 35 40 45
 Phe Leu Lys Gly Ile Thr Ala Ala Val Val Ile Asn Gly Ser Val Ala
 50 55 60
 Ala Val Gly Asn Thr Ile Ser Tyr Lys Asp Glu Thr Ile Pro Pro Val
 65 70 75 80
 Ser Leu Leu Arg Asn Gln Val Lys Met Thr Lys Asp Gly Leu Leu Asp
 85 90 95
 Val Val Glu Ala Leu Gln Ser Pro Leu Val Asp Lys Lys Ser Phe Ile
 100 105 110
 Pro Val Glu Arg Ser Asp Thr Thr Phe Leu Phe Leu Val Gly Gln Asp
 115 120 125
 Asp His Asn Trp Lys Ser Glu Phe Tyr Ala Asp Glu Ile Ser Lys Arg
 130 135 140
 Leu Gln Ala His Gly Lys Glu Lys Pro Gln Ile Ile Cys Tyr Pro Ala
 145 150 155 160
 Ala Gly His Tyr Ile Glu Pro Pro Tyr Phe Pro Leu Cys Ser Ala Gly
 165 170 175
 Met His Leu Leu Val Gly Ala Asn Ile Thr Phe Gly Gly Glu Pro Arg
 180 185 190
 Ala His Ala Val Ala Gln Val Asp Ala Trp Gln Gln Leu Gln Thr Phe
 195 200 205
 Phe His Lys Gln Leu Gly Ser Lys Ser Gly Ser His Pro Glu Thr Leu
 210 215 220
 Val Lys Val Lys Asp Ala Glu
 225 230

<210> 294
 <211> 623
 <212> DNA
 <213> Mus musculus

<400> 294
 gaattcgcg cggcgctcga cgaaacagga tctcccttct ctgctcagag atgagcaaat 60
 gccataatta cgacctcaag ccagcaaagt gggatacttc tcaagaacaa cagaaacaaa 120
 gattagcact aactaccagt caacctggag aaaatggtat cataagagga agatacccta 180

tagaaaaact caaaatatct ccaatgttcg ttgttcgagt ccttgctata gccttggcaa 240
 ttcgattcac ccttaacaca ttgatgtggc ttgccatttt caaagagacg tttcagccag 300
 tattgtgcaa caaggaagtc ccagtttcct caagagaggg ctactgtggc ccatgcccta 360
 acaactggat atgtcacaga aacaactgtt accaattttt taatgaagag aaaacctgga 420
 accagagcca agcttcctgt ttgtctcaaa attccagcct tctgaagata tacagtaaag 480
 aagaacagga tttcttaaag ctgggtaagt cctatcactg gatgggactg gtccagatcc 540
 cagcaaatgg ctctcggcag tgggaagatg gctcctctct ctcatacaat cagttaactc 600
 tggtggaat accaaaagga tcc 623

<210> 295

<211> 226

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (17)

<223> XAA = ANYTHING

<400> 295

Ala Ser Pro Ser Ile Ala Phe Leu Thr Ser Ser Ser Glu Leu Lys Lys
 1 5 10 15

Xaa Glu Ala Ile Arg Gly Arg Arg Arg Arg Asn Arg Ile Ser Leu Leu
 20 25 30

Cys Ser Glu Met Ser Lys Cys His Asn Tyr Asp Leu Lys Pro Ala Lys
 35 40 45

Trp Asp Thr Ser Gln Glu Gln Gln Lys Gln Arg Leu Ala Leu Thr Thr
 50 55 60

Ser Gln Pro Gly Glu Asn Gly Ile Ile Arg Gly Arg Tyr Pro Ile Glu
 65 70 75 80

Lys Leu Lys Ile Ser Pro Met Phe Val Val Arg Val Leu Ala Ile Ala
 85 90 95

Leu Ala Ile Arg Phe Thr Leu Asn Thr Leu Met Trp Leu Ala Ile Phe
 100 105 110

Lys Glu Thr Phe Gln Pro Val Leu Cys Asn Lys Glu Val Pro Val Ser
 115 120 125

Ser Arg Glu Gly Tyr Cys Gly Pro Cys Pro Asn Asn Trp Ile Cys His
 130 135 140

Arg Asn Asn Cys Tyr Gln Phe Phe Asn Glu Glu Lys Thr Trp Asn Gln
 145 150 155 160

Ser Gln Ala Ser Cys Leu Ser Gln Asn Ser Ser Leu Leu Lys Ile Tyr
 165 170 175

Ser Lys Glu Glu Gln Asp Phe Leu Lys Leu Val Lys Ser Tyr His Trp

180

185

190

Met Gly Leu Val Gln Ile Pro Ala Asn Gly Ser Trp Gln Trp Glu Asp
 195 200 205

Gly Ser Ser Leu Ser Tyr Asn Gln Leu Thr Leu Val Glu Ile Pro Lys
 210 215 220

Gly Ser
 225

<210> 296
 <211> 317
 <212> DNA
 <213> Mus musculus

<400> 296
 gaattcgagg ccgcgtcgac cagctgtgtg ctgccctgct tctgctcaac ctgatcttcc 60
 tcctagactc ctggattgag ctgtataata cccgaggttt ctgcattgcc gtggctgtat 120
 ttcttcaacta ttttctcttg gtctcattca catggatggg attagaagca ttccacatgt 180
 acctagcact ggtcaagggtg ttttaatactt acatccgaaa gtacatcctt aaattctgca 240
 ttgttggttg gggcatacca gctgtggttg tgtccatcgt cctgactata tccccagata 300
 actatgggat tggatcc 317

<210> 297
 <211> 232
 <212> PRT
 <213> Mus musculus

<220>
 <221> MOD_RES
 <222> (2)..(23)
 <223> XAA = ANYTHING

<400> 297
 Ile Xaa Thr Lys Ser Ile Arg Gly Ser Arg Gln Pro Asn Cys Ser Pro
 1 5 10 15

Gly Ser Arg Arg Ala Cys Xaa Thr Ala Arg Ile Ser Ser Pro Met Ala
 20 25 30

Met Pro Ala Cys Arg Ile Ser Trp Trp Lys Met Ala Ala Phe Leu Asp
 35 40 45

Ser Ser Thr Val Ala Gly Trp Val Trp Arg Thr Ala Ile Arg Thr Arg
 50 55 60

Trp Leu Pro Val Ile Leu Leu Lys Ser Leu Ala Ala Asn Gly Leu Thr
 65 70 75 80

Ala Ser Ser Cys Phe Thr Val Ser Pro Leu Pro Ile Arg Ser Ala Ser
 85 90 95

Pro Ser Ile Ala Phe Leu Thr Ser Ser Ser Glu Leu Lys Lys Glu Glu
100 105 110

Ala Ile Arg Gly Arg Val Asp Gln Leu Cys Ala Ala Leu Leu Leu Leu
115 120 125

Asn Leu Ile Phe Leu Leu Asp Ser Trp Ile Ala Leu Tyr Asn Thr Arg
130 135 140

Gly Phe Cys Ile Ala Val Ala Val Phe Leu His Tyr Phe Leu Leu Val
145 150 155 160

Ser Phe Thr Trp Met Gly Leu Glu Ala Phe His Met Tyr Leu Ala Leu
165 170 175

Val Lys Val Phe Asn Thr Tyr Ile Arg Lys Tyr Ile Leu Lys Phe Cys
180 185 190

Ile Val Gly Trp Gly Ile Pro Ala Val Val Val Ser Ile Val Leu Thr
195 200 205

Ile Ser Pro Asp Asn Tyr Gly Ile Gly Ser His Pro Glu Thr Leu Val
210 215 220

Lys Val Lys Asp Ala Glu Asp Gln
225 230

<210> 298

<211> 686

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (5)

<223> N = A, C, G OR T/U

<400> 298

tcttntagtt tgacaggcaa catcccaaaa acttttcgaa gcatttggtc agatcttcag 60
tattttccag ttttcataca gtctcggggt ttcaaacgt tgaaatcaag gacacgacgt 120
ttgcagtcta cctctgaaag attagtagaa gcacagaata tagcccatca tttgtgaagg 180
ggtttctttt gcgggacaga ggaacagatc ttgagagttt ggacaaactt atgaaaacta 240
aaaacatacc tgaagctcac caagatgcat ttaaaactgg ttttgcagag ggttttctca 300
aagctcaagc tcttacacag aagaccaatg attccttaag gcgaactcgt ctgatcctct 360
ttgttttgct cctgtttggc atttatggac tcttaaaaaa tccgttttta tctgtgcgct 420
ttcggacaac tacaggactt gattctgcgg tagaccctgt ccagatgaaa aatgtcactt 480
ttgaacatgt taaaggggtg gaggaagcca aacaagagtt acaggaagtg gttgaattct 540
tgaaaaatcc acagaagttt actgtgcttg gaggtaaact tcccaaagga attcttttag 600
ttggggccacc aggaacaggg aagacgcttc ttgcccagagc tgtggcagga gaagctgacg 660
tcccttttta ttatgcttct ggatcc 686

<210> 299

<211> 237

<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (1)
<223> XAA = ANYTHING

<400> 299
Xaa Phe Asp Arg Gln His Pro Lys Asn Phe Ser Lys His Leu Phe Arg
1 5 10 15
Ser Ser Val Phe Ser Ser Phe His Thr Val Ser Gly Phe Gln Asn Val
20 25 30
Glu Ile Lys Asp Thr Thr Phe Ala Val Tyr Leu Lys Ile Ser Arg Ser
35 40 45
Thr Glu Tyr Ser Pro Ser Phe Val Lys Gly Phe Leu Leu Arg Asp Arg
50 55 60
Gly Thr Asp Leu Glu Ser Leu Asp Lys Leu Met Lys Thr Lys Asn Ile
65 70 75 80
Pro Glu Ala His Gln Asp Ala Phe Lys Thr Gly Phe Ala Glu Gly Phe
85 90 95
Leu Lys Ala Gln Ala Leu Thr Gln Lys Thr Asn Asp Ser Leu Arg Arg
100 105 110
Thr Arg Leu Ile Leu Phe Val Leu Leu Leu Phe Gly Ile Tyr Gly Leu
115 120 125
Leu Lys Asn Pro Phe Leu Ser Val Arg Phe Arg Thr Thr Thr Gly Leu
130 135 140
Asp Ser Ala Val Asp Pro Val Gln Met Lys Asn Val Thr Phe Glu His
145 150 155 160
Val Lys Gly Val Glu Glu Ala Lys Gln Glu Leu Gln Glu Val Val Glu
165 170 175
Phe Leu Lys Asn Pro Gln Lys Phe Thr Val Leu Gly Gly Lys Leu Pro
180 185 190
Lys Gly Ile Leu Leu Val Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu
195 200 205
Ala Arg Ala Val Ala Gly Glu Ala Asp Val Pro Phe Tyr Tyr Ala Ser
210 215 220
Gly Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala
225 230 235

<210> 300
 <211> 705
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> (655)
 <223> N = A, C, G OR T/U

<400> 300
 cttcagcatc ttttactttc accagcggtt ctgggtggga tccgggggtgt gttactggca 60
 tctatggagt agatgtaagt aatggtgata aacagcctat aatgcacagc atagcctgac 120
 ccccaaaaaga agtatacatc ccagaatatc aatggtacag agattgagaa aactctcatt 180
 gagggcctag ttgtatttct tgttcaagac aagggttaca catttcaatt aagagagttc 240
 agctctacaa agaagtttta gtcgacgcgg ccgcgaattc aagcttactc ttcctttttc 300
 aattcagaag aactcgtcaa gaaggcgata gaaggcgatg cgctgcgaat cgggagcggc 360
 gataccgtaa agcacgagga agcggtcagc ccattcgccg ccaagctctt cagcaatatc 420
 acgggtagcc aacgctatgt cctgatagcg gtccgccaca cccagccggc cacagtcgat 480
 gaatccagaa aagcggccat tttccaccat gatattcggc aagcaggcat cgccatgggt 540
 cacgacgaga tcttcgccgt cgggcatgcg cgccttgagc ctggcgaaca gttcggctgg 600
 cgcgagcccc tgatgctctt cgtccagatc atcctgatcg acaaagaccg gcttncatcc 660
 gagtacgtgc tcgctcgatg cgatgtttcg cttggtggtc gaatg 705

<210> 301
 <211> 723
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> (600)..(707)
 <223> N = A, C, G OR T/U

<400> 301
 cttcgcacat tttactttca ccagcgtttc tgggtgggat ccgagcataa ataagacaga 60
 gaaaatccat ggatataagt attcttgcag gcaacaccac atagacattt agaaaattac 120
 ttaagtgttt tttgaatttt tactttacat gacttcatta attgtacttc cattaaagaa 180
 gagtttgtaa cacatctgta aacaaaaaag gcatatagca ttctattctt aatgaagaaa 240
 gaacatattt aaccacaaag taaaggaata atcacaataa aaagaagagc tttagctcat 300
 gaatatatat attgagttaa tgaataaata tatggtcgac gcggccgcga attcaagctt 360
 actcttcctt tttcaattca gaagaactcg tcaagaaggc gatagaaggc gatgcgctgc 420
 gaatcgggag cggcgatacc gtaaagcacg aggaagcggc cagcccattc gccgccaagc 480
 tcttcagcaa tatcacgggt agccaacgct atgtcctgat agcggtcgcg cacaccagc 540
 cggccacagt cgatgaatcc agaaaagcgg ccattttcca ccatgatatt cggcaagcan 600
 gcatcgccat gggtcacgac gagatcctcg ccgtcgggca tgcgcgcctt gagcctggcg 660
 aacagttcgg ctggcgcgag cccctgatgc tcttcgtcca gatcatnctg atcggcaaga 720
 ccg 723

<210> 302
 <211> 610
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (495) .. (571)
 <223> N = A, C, G OR T/U

<400> 302
 ggatccacag agtgccgggt cccctgccac cactttctgg gagcttttct ctgtagtacc 60
 caggagcaca gtcctgacag gagggtcctg cggtgccagg aggacagaca cagagctcca 120
 acagcaatgc cgcctcgccc tcagcgggca gctcgacagc tttccggcca acctccatgg 180
 aaatgtttggc aattctgctc tgctgcagtc cctggccgta tgatgctttg atgaggatgt 240
 agtcaatatt gctgagaaca gacataaaat cagagtgtgt gacgtgtttc tcagacacgg 300
 agttaaaata tttccagaat tcaagcttac tcttcctttt tcaattcaga agaactcgtc 360
 aagaaggcga tagaaggcga tgcgctgcga atcgggagcg gcgataccgt aaagcacgag 420
 gaagcgggtca gccattcgc cgccaagctc ttcagcaata tcacgggtag ccaacgctat 480
 gtccctgatag cggtnccgca caccagccg gccacagtcg atgaatccag aaaagcggtc 540
 attttccacc atgatattcg gcaagcaggc ntcgccatgg gtcacgacga agatcctcgc 600
 ccgtccggcg 610

<210> 303
 <211> 606
 <212> DNA
 <213> Mus musculus

<400> 303
 ggatcccaat acttcgacca ggtgaccccc tggtaaattgt gtgtaagaca tctacaaaat 60
 cagcgtcatc aggagaaagg cgactggggg cttctgcata ctcaaagtta ggcccagctg 120
 gatccgaaca accataacca tccagaaatt ttcttctggg tcattgaaga actgtctgtt 180
 cttctgtgtg tgtaaagatt ttgcagggtt cgatgggcta aaagtccttg taaactgtac 240
 aattgcttca cataatccaa catttctaatt tttttcattc ttttctactt catttgatg 300
 gtaaaacaga attttatttt ctctctctcc cccgcggggc cgaattcaag cttactcttc 360
 ctttttcaat tcagaagaac tcgtcaagaa ggcgatagaa ggcgatgcgc tgcgaatcgg 420
 gagcggcgat accgtaaaagc acgaggaagc ggtcagccca ttcgcccga agctcttcag 480
 caatatcacg ggtagccaac gctatgtcct gatagcggtc cgccacacc agccggccac 540
 agtcgatgaa tccagaaaag cggccatttt ccaccatgat attcggcaag caggcatcgc 600
 catggg 606

<210> 304
 <211> 608
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (589)
 <223> N = A, C, G OR T/U

<400> 304
 ggatcccaat cctgctgctg gagggtcttc gcaaaccctt gctgtgcctt ggaaaaaagt 60
 gcccaagctg ctgacgcaaa aagaaaaaaa aaaagaaaga aagatgctgc tcatttgcac 120
 gctcacttac atatatttgc atgttcaactg acccagcctg agctctcccc agcctcgtgg 180
 gtgggtgactt ttctctcagg gcgcacgccc tgctgcagcc cctcccccg cggggcccgaa 240
 ttcaagctta ctcttccttt ttcaattcag aagaactcgt caagaaggcg atagaaggcg 300

```

atgcgctgcg aatcgggagc ggcgataccg taaagcacga ggaagcggtc agcccattcg 360
ccgccaagct cttcagcaat atcacgggta gccaacgcta tgtcctgata gcggtccgcc 420
acaccagcc ggccacagtc gatgaatcca gaaaagcggc cttttccac catgatattc 480
ggcaagcagg catcgccatg ggtcacgacg agatcctcgc cgtcgggcat gcgcgccttg 540
agcctggcga acagttcggc tggcgcgagc ccctgatgct cttcgtcana tcatcctgat 600
cgacaagg                                     608

```

<210> 305

<211> 635

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (596)..(635)

<223> N = A, C, G OR T/U

<400> 305

```

ggatcccaat cctgctgctg gagtgtcttc gcaaaccctt gctgtgcctt ggaaaaaagt 60
gcccaagctg ctgacgcaaa aagaaaaaaa aaaagaaaga aagatgtctg tcatttgcac 120
gctcacttac atatatttgc atgttctactg acccagcctg agctctcccc agcctcgttg 180
gtggtgactt ttcttgacag gcgcacgccc tgtgcagcc cctcccccg cgggcccga 240
ttcaagctta ctcttctttt ttcaattcag aagaactcgt caagaaggcg atagaaggcg 300
atgcgctgcg aatcgggagc ggcgataccg taaagcacga ggaagcggtc agcccattcg 360
ccgccaagct cttcagcaat atcacgggta gccaacgcta tgtcctgata gcggtccgcc 420
acaccagcc ggccacagtc gatgaatcca gaaaagcggc cttttccac catgatattc 480
ggcaagcagg catcgccatg ggtcacgacg agatcctcgc cgtcgggcat gcgcgccttg 540
agcctggcga acagttcggc tggcgcgagc ccctgatgct cttcgtccag atcatnctga 600
tcgacaagac cggctttcat tccgagtacg tgctn                                     635

```

<210> 306

<211> 635

<212> DNA

<213> Mus musculus

<400> 306

```

ggatcccacg gggaaagggtg gcacagggtg tatttgtgaa tgccacggac ccggtgtcga 60
ttccatctcc tgcactggca tggcaactat ctgcaacatg ggtgcagaaa ttggggccac 120
tacatcagtg ttcccatata accacaggat gaaaaagtac ctgagcaaga caggccgaac 180
agacattgcc aacctagcag aagaattcaa gcttactctt ctttttcaa ttcagaagaa 240
ctcgtcaaga aggcgataga aggcgatgcg ctgcgaatcg ggagcggcga taccgtaaag 300
cacgaggaag cggtcagccc attcgccgcc aagctcttca gcaatatac gggtagccaa 360
cgctatgtcc tgatagcggc ccgccacacc cagccggcca cagtcgatga atccagaaaa 420
gcggccattt tccaccatga tattcggaac gcaggcatcg ccattgggtc cgacgagatc 480
ctcgccgtcg ggcagtcgcg ccttgagcct ggccaacaag ttcggctggc gcgagccctt 540
gatgctcttc gtccagatca tcctgatcga caaagaccgg ctttcatccg agtacctgct 600
cgctcgatgc gatgtttcct tggggggcga atggg                                     635

```

<210> 307

<211> 635

<212> DNA

<213> Mus musculus

<400> 307

```
ggatccctcg gtgaaagggtg gcacagggtgc tattgtggaa taccacggac ccggtgtcga 60
ttccatctcc tgcactggca tggcaactat ctgcaacatg ggtgcagaaa ttggggccac 120
tacgtcagtg ttcccataca accacaggat gaaaaagtac ctgagcaaga caggccgaac 180
agacattgcc aacctagcag aagaattcaa gcttactctt cctttttcaa ttcagaagaa 240
ctcgtcaaga aggcgataga aggcgatgcg ctgcgaatcg ggagcggcga taccgtaaag 300
cacgaggaag cggtcagccc attcgccgcc aagctcttca gcaatatcac gggtagccaa 360
cgctatgtcc tgatagcggc ccgccacacc cagccggcca cagtcgatga atccagaaaa 420
gcgccattt tccaccatga tattcggaac gcaggcatcg ccatgggtca cgacgagatc 480
ctcgccgtcg ggcattgcgc ccttgagcct ggccaacagt tgggctggcg cgagcccctg 540
atgctcttcg tccagatcat cctgatcgac aagaccggct ttcattccga gtacgtgctc 600
gctcgatgcg atgtttcgct tgggtggtcga atggg 635
```

<210> 308

<211> 635

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (524)

<223> N = A, C, G OR T/U

<400> 308

```
ggatccctgc ggccactgcc cagagagaat cgttacaatc acaggcccaa ctgacgccat 60
cttcaaggcc tttgctatga tcgcgtacaa gtttgaggag gacatcatta attccatgag 120
caacagcccc gccccgcggg gcccgaattc aagcttactc ttcctttttc aattcagaag 180
aactcgtaaa gaaggcgata gaaggcgatg cgctgcgaat cgggagcggc gataccgtaa 240
agcacgagga agcggtcagc ccattcgccg ccaagctctt cagcaatatc acgggtagcc 300
aacgctatgt cctgatagcg gtccgccaca cccagccggc cacagtcgat gaatccagaa 360
aagcggccat tttccaccat gatattcggc aagcaggcat cgccatgggt cacgacgaga 420
tcctcgccgt cgggcatgcg cgccttgagc ctggcgaaca gttcggctgg cgcgagcccc 480
tgatgctctt cgtccagatc atcctgatcg acaagaccgg cttncatccg agtacgtgct 540
cgctcgatgc gatgtttcgc ttggtggtcg aatgggcagg tagccggatc aaagcgtatg 600
cagcccgcgg cattgcatca gccatgatgg atact 635
```

<210> 309

<211> 631

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (580)..(597)

<223> N = A, C, G OR T/U

<400> 309

```
ggatccgaca ccgtcttctg gcttccacag gcgcccattc acaatgtgtg gcacacatat 60
ctagaaacat agacatatga agaaaataaa aataactcgg tagagctggg cattgtggta 120
catattttta gtccatagcat ttgggagaca acagaaagcg gagcgtgtg ggctcaaatc 180
tagcctgata cacatgggtga gtgagttcta ggccaaccga ggatgagaac ttgtctcaaa 240
acagttttta aagaaaatac tctagaataa aacagaacta agcaccacca ccagtagagt 300
```

```

gcacagaaat aagacacact ggtgctgaat atttcatagc ctgtgtgtgt ctgtccttcc 360
tttcctttat gttttttttt gagacagggt ttctctgtgt agccctggct gttctggaac 420
tcaactctga gaccatgctg gcctcaaact cagaaatttg cctgcctctg cctcccaagt 480
gctgaaatga aagggtgtgt cactacgtgt ttcttttctt ttttaattaac taattaatta 540
acatctcaaa cactggctcc cccttcgtgg taccctctn acagagtccc ttccctnccc 600
tctttctttc tctgtgaga gtgtgcccgc g 631

```

```

<210> 310
<211> 603
<212> DNA
<213> Mus musculus

```

```

<220>
<221> modified_base
<222> (512) .. (597)
<223> N = A, C, G OR T/U

```

```

<400> 310
ggatccgacc ccctgccgtt ctctatgtgc ttctatgagg gttactatga tgaaaataga 60
gcagaagata gtgtgaagta acattggcaa ctgtaatgtg tccatttaac ttatttttat 120
agcacttagg caatattgtt agtcttagtg agtagttcac atctttacaa aagcatgctc 180
tccctatcca ttggggccac aataacactc tctttgaggg cattctgaat cctgtctcgt 240
gtaacgataa tatattatga aaacagatac ttttaagaatt tctgtacag cagtcagttg 300
tttattctct ctctctctct ctctctctct ctctctctct ctctctctct ccctcgggcc 360
caatcccgcg ggctgaatt caagcttact ctcccttttt caattcagaa gaactcgtca 420
agaaggcgat agaaggcgat gcgctgcaa tggggagcgg cgataccgta aagcacgagg 480
aagcggtcag ccatttcgcc gccaaagctt tnagcaatat cacgggtagc caacgctatg 540
tctgatagc ggccgncaca ccagccggn cacagtcgat gaatccagaa aagcggncat 600
ttt 603

```

```

<210> 311
<211> 608
<212> DNA
<213> Mus musculus

```

```

<220>
<221> modified_base
<222> (489) .. (596)
<223> N = A, C, G OR T/U

```

```

<400> 311
ggatccgcat ggcatgtgat cgatttgga cattgcaacc aacaagctga ccttctccta 60
ctccttcaag atgaagatgt ctgttatcct cggcatcatc cacatgctgt ttggagtcag 120
cctgagcctt ttcaaccata tctatttcaa gaagcccctg aacatctact ttggctttat 180
tcttgagatc atcttcatgt cctcgttgtt tggctacctg gtcacctta tcttttacia 240
gtggacagcc tacgatgccc actcgtctag gaatgccccg agcctcctga tccacttcat 300
aaacatgttc ctcttctcct acccagagtc tggtaatgca atgctgtact ctggacagaa 360
aggaattcaa gcttactctt cctttttcaa ttcagaagaa ctcgtaaga aggcgataga 420
aggcgatgag ctgcgaatcg ggagcggcga taccgtaaag cacgaggaag cggtcagccc 480
attcgccgnc aagctctttc agcaatatca cgggtagcca acgctatgtc ctgatagcgg 540
gccgccacac ccagccgggc acaggtcgat gaattcagaa aagcgggcca tttttncacc 600
atgatatt 608

```


<210> 312
 <211> 637
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (117)..(627)
 <223> N = A, C, G OR T/U

<400> 312
 ggatccgccg ggggtcagaa gccatggagt cagcattatc accaaggata ttattgaata 60
 cccaaataaa acgaactgat acatatttct ccaaaacctt cacaagaagt cgactgnttt 120
 ctttagtagg ctaacttttt aaacattcca caagaggaag tgcccgcggg cctgaattca 180
 agcttactct tcctttttca attcagaaga actcgtcaag aaggcgatag aaggcgatgc 240
 gctgcgaatc gggagcggcg ataccgtaaa gcacgaggaa gcggtcagcc cattcgccgc 300
 caagctcttc agcaatatca cgggtagcca acgctatgtc ctgatagcgg tccgccacac 360
 ccagccggcc acagtcgatg aatncagaaa agcggncatt ttccaccatg atattcggca 420
 agcaggcatc gccatgggtc acgacgagat cctcgccgtc gggcatgcgc gccttgagcc 480
 tggcgaacag ttcggtctggc gcgagcccct gatgctcttc gtccagatca tcctgatcga 540
 caaagaccgg nttncatccg agtaccgtgc tcgctcgatg cgangtttcg cttggnggtn 600
 naatgggcag gttagnccgg atcaagncta tgcagcc 637

<210> 313
 <211> 607
 <212> DNA
 <213> Mus musculus

<400> 313
 ggatccggca ggaagaggcc aggcagatgc agaagcagca gcagcagcaa caacaacaac 60
 aacagcaaca ccagcaatca aacagagccc ggaacagcac acattccaac ctgcatacca 120
 gccttgggaa ttcaagctta ctcttccttt ttcaattcag aagaactcgt caagaaggcg 180
 atagaaggcg atgcgctgcg aatcgggagc ggcgataccg taaagcacga ggaagcggtc 240
 agcccattcg ccgccaagct cttcagcaat atcacgggta gccaacgcta tgtcctgata 300
 gcggtccgcc acaccagacc ggccacagtc gatgaatcca gaaaagcggc cattttccac 360
 catgatattc ggcaagcagg catcgccatg ggtcacgacg agatcctcgc cgtcggggcat 420
 gcgcgccttg agcctggcga acagttcggc tggcgcgagc cctgatgct cttcgtccag 480
 atcatcctga tcgacaagac cggcttcacg cgagtacgtg ctgctcgat gcgatgtttc 540
 gcttggtggt cgaatgggca ggtagccgga tcaagcgtat gcagccgccg cattgcatca 600
 gccatga 607

<210> 314
 <211> 633
 <212> DNA
 <213> Mus musculus

<400> 314
 ggatccggtc agaagccatg gagtcagcat tatcaccaag gatattattg aatacccaaa 60
 taaaacgaac tgatacatat ttctccaaa ctttcacaag aagtcgactg ttttctttag 120
 taggctaact ttttaaacat tccacaagag gaagggcccg cgggcccga tcaagctta 180
 ctcttccttt ttcaattcag aagaactcgt caagaaggcg atagaaggcg atgcgctgcg 240
 aatcgggagc ggcgataccg taaagcacga ggaagcggtc agccattcg ccgccaagct 300

```

cttcagcaat atcacgggta gccaacgcta tgtcctgata gcggtccgcc acaccagcc 360
ggccacagtc gatgaatcca gaaaagcggc cttttccac catgatattc ggcaagcagg 420
catcgccatg ggtcacgacg agatcctcgc cgtcgggcat gcgcgccttg agcctggcga 480
acagttcggc tggcgcgagc ccctgatgct cttcgtccag atcatcctga tcgacaagac 540
cggcttccat ccgagtacgt gctcgtcga tgcgatgttt cgcttggtgg tcgaatgggc 600
aggtagccgg atcaagcgta tgcagccgc cgc
633

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<210> 315

<211> 631

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (7)..(631)

<223> N = A, C, G OR T/U

<400> 315

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ggatccnttg ngggnnatna ccnnnggagn naccatnatn annaaggata tnatatgaat 60
acccaagatc attggncntg atgngtatgt tctnnacaac ctntatatga ancagactgc 120
nnntntnat nngcnaantt nnnnaanngtt acncaagang aantgtcct tnnccnatat 180
tcaagntnnc tnttcntttg tnanatnaagn ngancnctg nanatngcga nccaaggtgn 240
ngcgtgcnn annngnancg gcnatccctt nnannacgag gnatnggnca gtctattngc 300
nggccanctc tttntcntna tnnccgggtcg ccannnctat gngctnanag cggatnmana 360
cacncangcg gccannntcc atnatnanat nnnngcggcc ntntccacc nngatntnna 420
nnagnnnctc atcgtcatgn ntgcnacctn ntccctggcg accngcatgc gctgctngag 480
ccngtgatnc agttcggctg gancnngctn ntgangctgt tcgncntgan tatcctganc 540
nacatgatcg gtnngatgen agttcgngct cgctntntgc gatgtttccg ttgaaggngct 600
antgggcngg tnnattggat caagccattg n
631

```

<210> 316

<211> 607

<212> DNA

<213> Mus musculus

<400> 316

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ggatcctaac ctacacagctg aaagcagcca tagcagaatg caggccagag aacgaacttt 60
agaaataacc cacctacttg tgtctgggga attcaagctt actcttcctt tttcaattca 120
gaagaactcg tcaagaaggc gatagaaggc gatgcgctgc gaatcgggag cggcgatacc 180
gtaaagcacg aggaagcggg cagcccattc gccgccaagc tcttcagcaa tatcacgggt 240
agccaacgct atgtcctgat agcgggtccgc cacaccagc cggccacagt cgatgaatcc 300
agaaaagcgg ccattttcca ccatgatatt cggcaagcag gcatcgccat gggtcacgac 360
gagatcctcg ccgtcgggca tgcgcgcctt gagcctggcg aacagttcgg ctggcgcgag 420
cccctgatgc tottcgtcca gatcactctg atcgacaaga ccggttcca tccgagtacg 480
tgctcgctcg atgcgatgtt tcgcttggtg gtcgaatggg caggtagccg gatcaagcgt 540
atgcagccgc cgcattgcat cagccatgat ggatacttcc tcggcaggag caaggtggga 600
tgacagg
607

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<210> 317

<211> 225

<212> DNA

<213> Mus musculus

<220>
 <221> modified_base
 <222> (13)..(204)
 <223> N = A, C, G OR T/U

<400> 317
 ggatcctcac tgnncggcaa aatgccgcaa aaaaggggaat aagggcgaca cggaaatgtt 60
 gaatactcat actcttcctt tttcaatatt attgaagcat ttatcagggg tattgtctca 120
 tgagcggata catatttgaa tgtattctgc agaagaacat gtgagcaaaa ggccagcnaa 180
 aggcctnnaa ccggaataag gccnccgtgc tggctttttt ccata 225

<210> 318
 <211> 633
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (8)..(630)
 <223> N = A, C, G OR T/U

<400> 318
 ggatcctnac tgnncggcaa ancgccgcaa aaaaggggaat gggggctgac acgganatgt 60
 ttgaatactc atactcttcc tttnttanta ttnttgaann nttntcnng nntattggnt 120
 natgagcggg tacntatttg aatgtattct gcataagaac atgtgagcaa aagggcagca 180
 naagggcngg aaccggaaaa aggcgcnggt gctggcggtt ttccataggc tccgaccccc 240
 tgacgagcat canaaaaatc gacgctcaat tcagatgtgg caaaccgcac tggactataa 300
 agataccagg cgttttacccc tgnnancctc ctagtncgct ntccctgttc gncctgccg 360
 cttaccggat acctgtccgc ctttctccct tcgggaagcg tggcgctttc tcatagctca 420
 cgctgtatgt ntctcangtc ggtgtaggta ngntcgctcc aatctgggct gngtgcacga 480
 accnccggt cancccgacc gctgngcctt atccggaaac tatctatttg agttcacccg 540
 gnaagacacc acttatnttc ctgcagnagn cactggtnac atgattatna nancgaggtt 600
 tttngcngg tctncaagnn ttctttgaan ttt 633

<210> 319
 <211> 645
 <212> DNA
 <213> Mus musculus

<400> 319
 tcttcagcat cttttacttt caccagcggt tctgggtggg atccaaagcc tccaattatt 60
 attggtatta ctatgaagaa aattataaca aaagcatggg cagttacgat aacattgtaa 120
 atttggtcat ctctaaaaag tgcacctggg tgacctaat ctgctcgaat taaaatactt 180
 agtgcagtac ccactattcc cgcggggccc aattcaagct tactcttcct ttttcaattc 240
 agaagaactc gtcaagaagg cgatagaagg cgatgcgctg cgaatcggga gcggcgatac 300
 cgtaaagcac gaggaagcgg tcagcccatc cgccgccaa gctcttcagca atatcacggg 360
 tagccaacgc tatgtcctga tagcgggtccg ccacaccag ccggccacag tcgatgaatc 420
 cagaaaagcg gccattttcc accatgatat tcggcaagca ggcacgcga tgggtcacga 480
 cgagatcctc gccgtcgggc atgcgcgcct tgagcctggc gaacagttcg gctggcgcca 540
 gccctgatg ctcttcgtcc agatcatcct gatcgacaag accggcttcc atccgagtac 600
 gtgctcgctc gatgcgatgt ttcgcttggt ggtcgaatgg gcagg 645

<210> 320
 <211> 289
 <212> DNA
 <213> Mus musculus

<400> 320
 gaattcgcgg ccgcgtcgac gccaaagactt cacacagttc tgattgtccc agaagccttg 60
 cgtttgtcaa aacatgacaa tgagatatga aaacttccag aacttggagc gggaagagaa 120
 aaaccaggag atgagaaatg gtgacaagaa aggaggaatg gagtctccaa agtttgtctt 180
 aattccttcc cagtccttcc tgtggcgcat cctctcttgg acccacctcc tctgtttctc 240
 cctgggcctc agcctcctgc tactgggtgt catctccgtg attggatcc 289

<210> 321
 <211> 684
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (124)..(153)
 <223> N = A, C, G OR T/U

<400> 321
 acctcagtga tgtgcaaggg tgatcaatga tcgggtgagtc tctctcatct cagtgtgtgg 60
 agtgcaagag tagagaaactc agatgccaac taattcttga gcatggataa ccaaatttca 120
 ggggnaggagc cgttttcaat agctaaaagt gcntgagtta taatcacctt gtcacgtttt 180
 gggttgggttc tgaatttgca taccaaccag agcatgaaca ccagtccaca gcatatggca 240
 gcaccaaaca aaatcactcc caccatttcc ttaaagtaag aaaaagcaga ggtaagccaa 300
 gaggtaaagt ctccgagggg cactgggttcc actctggtcc cattaaggct caggatctgc 360
 atctgcagtc tcgtctgcaa cctttccagc tctgctgacc agttcccctt caggtaactc 420
 gataggtctg tacttttaat aaaagaatta ttaatatacc tattgggagt aatgcacaca 480
 tgcaaagtgg atgccacaca actcatttgt atgacatcca tcactctgtc catgtcatgt 540
 tgtaaaatat ccaactctgat tcaactaacat taaccctgag gtgatatgag aatccaccct 600
 ttgcagggtg agcaatgcct cagacgtttt ttctgctatc tgacttatag tgtcagcagt 660
 attaatttga tctgcccttg atcc 684

<210> 322
 <211> 719
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> (628)..(666)
 <223> N = A, C, G OR T/U

<400> 322
 cttcagcatc ttttctttca ccagcgtttc tgggtgggat ccaggggtgg ggtggaaaaac 60
 ttgctaaaaa caaagcaaat gtctttcaat attcacaacc ttaaaattat atccaagaaa 120
 acaaaggata aataattttt tataaaaata attacttctc aaataacgtt tcacaataga 180
 cctgtctaat acatcgatct gactcatctc atctgtgccc cttttcttct ttttaaaatt 240
 ctggcctggg acaaaactac atgaaagaaa gtaccattaa attaaggggt actttccaaa 300

aaacaataga aaaatcttaa aagtaaattc acttatatat aaaatattaa ggcctctgca 360
 tgagaacggt ttaacatctg gggaactggc ctttcctaac tgacctatga cccactcac 420
 ctcaaacttc agaataaag gttctggagt gaaaagtcct ttaattttg ccaatacatg 480
 aaattacaca taaaattaca ctgcaaagta atatgtactt aacaaatgat atattgaaaa 540
 gtctaacttt ctgctggcta atttcagtat ggacttcaga tcaagtatag tgtattttca 600
 gccatatctc ataatctttt gcgacgcngn cgcaattca agcttactct tnccttttca 660
 attcanaaga actcgtcaag aaggcgatag aaggcgatgc gctgcgaatc gggagccgg 719

<210> 323

<211> 655

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (16)..(85)

<223> N = A, C, G OR T/U

<400> 323

gttgtagatc tgaaancaag aaagaaggcg gggcttgagg tectgaggtc acttaagggc 60
 caccntnttt gacntaagac ctcantaggc cccgcctcta aaggtttctg acctcaatag 120
 gccttcctgg agaactagtt tctaactctc aggccttgag gacattgcat ctgagtagta 180
 ggtgcctctc tacctgtggt tggcttggtc atgattggca gacactctgc ctggctctgc 240
 acagcagcgg ctcagcatca gcattccagct gcttgctgtg tgtagttgt ctacagctg 300
 agggctctgc ctgcgctact tcaggctttc cggttaggaa gataatttg tcacttgtgt 360
 ctgtggccac tcttagaatt ttctcttttg agggaaacctg tgactgggtg gcttttgcac 420
 tctatggagg gagatggggt taaagactgt ggcaacacac accctccaga agagctggga 480
 ccagagactg tcagcacaga aaggacaatg tcttttttag tagctgtggc agacttgagt 540
 tgctgtaatt tatacaaatt gtttagaatg gtttttaaga ctaagaaggg aaatatactt 600
 attgcacaag acttttataa ttactatact taaattatgc tctatgtggg gatcc 655

<210> 324

<211> 677

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> (1)

<223> N = A, C, G OR T/U

<400> 324

ncgctgtagt ttcatttctc actttgaggg cacagatgaa aatgtatatc gcaacacagt 60
 ggatatcagc ccaagcacga agaccatgct gaacatgcac ccgtacagag tgtacttaaa 120
 ggagtcgtca taagggcact gggagccatt ggagcttacc attgtcaggc agtgcagctt 180
 acaggaggcc ttttgtccgc agcgcttgat cgatgcgctt tgctattcag atgtgggtcac 240
 agcagcagcc agtttatgtg caaagtattt gtttcttttc ctgttcttac aaatactttc 300
 ttctcttaac tcttcaaagg aaacatgaaa tgtgttccgt aaaagtctct agtagattat 360
 tcaggaaaat agtctgattt tctggtcgag aaaatccatg agtctggagt ttagttaact 420
 gacagaaaat gcagtcaagg aagccaaccc ataaagctga aagtgtagg aaaaactggt 480
 ccaagtcgga ccagaccagt ccgcgtggaa acttgtgctt cagccgccag ggtccaaacc 540
 agctttactt cagtcacaaa cactgcgcgt gcgtccgtcc gccgctcgtc ctccgggtact 600
 tcttccttct ttttattctc aaactttgta tttctacatt gattccggac ggcgataggc 660

